STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 118660

TO: Nancy Vogel
Location: rem/2a65/2c70
Art Unit: 1636
Wednesday, April 07, 2004

Case Serial Number: 10/032393

From: Mary Jane Ruhl
Location: Biotech-Chem Library
Remsen 1-B55
Phone: 571-272-2524

maryjane.ruhl@uspto.gov

Search Notes

Examiner Vogel,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl
Technical Information Specialist
STIC
CM-1, Rm. 6-A-06
605-1155

Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.
Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions **.rnpm** and **.rnpn**
Searches run against the Amino Acid Pending database produce two sets of results, with the extensions **.rapm** and **.rapn**

Because they contain data that is confidential, the results of Pending database searches should not be left in the case .

USPTO

STIC SEARCH RESUL FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact ***the searcher or contact***:

Mary Hale, Information Branch Supervisor
571-272-2507 Remsen E01 D86

Voluntary Results Feedback Form

- *I am an examiner in Workgroup:* ☐ *Example: 1610*
- *Relevant prior art **found**, search results used as follows:*
  - ☐ 102 rejection
  - ☐ 103 rejection
  - ☐ Cited as being of interest.
  - ☐ Helped examiner better understand the invention.
  - ☐ Helped examiner better understand the state of the art in their technology.

  Types of relevant prior art found:
  - ☐ Foreign Patent(s)
  - ☐ Non-Patent Literature
    (journal articles, conference proceedings, new product announcements etc.)
- *Relevant prior art **not found**:*
  - ☐ Results verified the lack of relevant prior art (helped determine patentability)
  - ☐ Results were not useful in determining patentability or understanding the invention

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library Remsen Bldg.

sira
Search and Information Resources Administration

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 7, 2004, 03:17:56 ; Search time 1681 Seconds
(without alignments)
1314.988 Million cell updates/sec

Title: US-10-032-393-36
Perfect score: 51
Sequence: 1 tcataaaaaatttatttgct.....ttttctgtataatagattca 51

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	51	100.0	60	6	A15398	A15398 Synthetic P
	2	51	100.0	75	7	PT5PN25	M11602 Bacteriopha
	3	51	100.0	202	6	A10374	A10374 Nucleotide
	4	51	100.0	202	6	A11246	A11246 vector pDS2
	5	51	100.0	202	6	E00936	E00936 DNA sequenc
	6	51	100.0	207	6	A10375	A10375 Nucleotide
	7	51	100.0	247	6	A11242	A11242 vector pDS1
	8	51	100.0	259	6	A10373	A10373 Nucleotide
	9	51	100.0	1113	6	A02739	A02739 Artificial
	10	51	100.0	1113	6	A14592	A14592 Synthetic n
	11	51	100.0	1221	6	A02296	A02296 Plasmid pDS
	12	51	100.0	1221	6	A14593	A14593 Synthetic n
	13	51	100.0	1866	6	A02227	A02227 Plasmid pDS
	14	51	100.0	1866	6	A02295	A02295 Plasmid pDS
	15	51	100.0	1866	6	A02740	A02740 Artificial
	16	51	100.0	1866	6	A07053	A07053 Nucleotide
	17	51	100.0	1866	6	A14594	A14594 Synthetic n
	18	51	100.0	3403	6	A02228	A02228 Plasmid pDS
	19	51	100.0	5767	6	AX035965	AX035965 Sequence
	20	51	100.0	6000	12	U66308	U66308 Expression
	21	51	100.0	6447	12	AF288421	AF288421 Synthetic
	22	50	98.0	76	6	A11173	A11173 A T5 promot
	23	46.4	91.0	524	12	SYNIFNGS	K01699 Human immun
	24	46	90.2	73	6	A12013	A12013 oligonucleo
c	25	46	90.2	73	6	A12014	A12014 oligonucleo
	26	42.8	83.9	83	6	A16630	A16630 Nucleotide
c	27	42.8	83.9	83	6	A16631	A16631 Nucleotide
	28	39	76.5	68	6	E01976	E01976 DNA encodin
	29	33.6	65.9	131	6	A50146	A50146 Sequence 3
	30	33.4	65.5	125	6	A46760	A46760 Sequence 2
	31	33.4	65.5	125	6	I89341	I89341 Sequence 2
	32	33	64.7	116	6	A13088	A13088 Nucleotide
	33	33	64.7	132	12	SYNADRE1B1	M16661 Synthetic a
	34	33	64.7	171	6	AR069843	AR069843 Sequence
	35	33	64.7	173	6	A01257	A01257 Nucleotide
c	36	33	64.7	173	6	A01258	A01258 (reverse co
	37	33	64.7	173	6	A13104	A13104 Nucleotide
c	38	33	64.7	173	6	A13105	A13105 Nucleotide
	39	33	64.7	180	6	A01247	A01247 Nucleotide
c	40	33	64.7	180	6	A01248	A01248 (reverse co
	41	33	64.7	180	6	A13094	A13094 Nucleotide
c	42	33	64.7	180	6	A13095	A13095 Nucleotide
	43	33	64.7	319	12	ARLACI	X06035 Synthetic l
	44	33	64.7	396	6	A11819	A11819 Artificial
c	45	33	64.7	396	6	A11820	A11820 Artificial

ALIGNMENTS

RESULT 1
A15398
LOCUS A15398 60 bp DNA linear PAT 22-SEP-1995
DEFINITION Synthetic Phage T5 promoter P-N 25.
ACCESSION A15398
VERSION A15398.1 GI:1247805
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 60)
AUTHORS Bujard,H. and Le Grice,S.
TITLE New gram-positive expression control sequences

```
FEATURES             Location/Qualifiers
     source          1. .60
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             100.0%;  Score 51;  DB 6;  Length 60;
  Best Local Similarity   100.0%;  Pred. No. 0.0089;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51


RESULT 2
PT5PN25
LOCUS       PT5PN25                   75 bp    DNA     linear   PHG 28-APR-1993
DEFINITION  Bacteriophage T5 promoter P-N 25.
ACCESSION   M11602
VERSION     M11602.1  GI:215985
KEYWORDS    promoter region.
SOURCE      Bacteriophage T5
  ORGANISM  Bacteriophage T5
            Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
            T5-like viruses.
REFERENCE   1  (bases 1 to 75)
  AUTHORS   Gentz,R. and Bujard,H.
  TITLE     Promoters recognized by Escherichia coli RNA polymerase selected by
            function: highly efficient promoters from bacteriophage T5
  JOURNAL   J. Bacteriol. 164 (1), 70-77 (1985)
  MEDLINE   86008105
   PUBMED   3900050
COMMENT     Original source text: Bacteriophage T5 DNA.
FEATURES             Location/Qualifiers
     source          1. .75
                     /organism="Bacteriophage T5"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10726"
     misc_RNA        56. .>75
                     /note="bacteriophage T5 RNA"
ORIGIN      Undetermined.

  Query Match             100.0%;  Score 51;  DB 7;  Length 75;
  Best Local Similarity   100.0%;  Pred. No. 0.0085;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 56


RESULT 3
A10374
LOCUS       A10374                   202 bp    DNA     linear   PAT 22-SEP-1993
DEFINITION  Nucleotide sequence 21 from patent number EP0303925.
ACCESSION   A10374
VERSION     A10374.1  GI:490696
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 202)
  AUTHORS   Bujard,H. and Lanzer,M.
  TITLE     High repressible sequence for control of expression
  JOURNAL   Patent: EP 0303925-A 21 22-FEB-1989;
            F. HOFFMANN-LA ROCHE AG
FEATURES             Location/Qualifiers
     source          1. .202
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             100.0%;  Score 51;  DB 6;  Length 202;
  Best Local Similarity   100.0%;  Pred. No. 0.0068;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 174


RESULT 4
A11246
LOCUS       A11246                   202 bp    DNA     linear   PAT 12-NOV-1993
DEFINITION  vector pDS2/PN25x/0,to2+ XhoI/EcoRI fragment.
ACCESSION   A11246
VERSION     A11246.1  GI:491020
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 202)
  AUTHORS   Bujard,H. and Stueber,D.
  TITLE     New expression control sequence
  JOURNAL   Patent: EP 0186069-A 10 02-JUL-1986;
            F. HOFFMANN-LA ROCHE AG
FEATURES             Location/Qualifiers
     source          1. .202
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             100.0%;  Score 51;  DB 6;  Length 202;
  Best Local Similarity   100.0%;  Pred. No. 0.0068;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 174


RESULT 5
E00936
LOCUS       E00936                   202 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  DNA sequence including promoter and operator hybrid 'P(N25X/)'.
ACCESSION   E00936
VERSION     E00936.1  GI:2169197
KEYWORDS    JP 1986181386-A/1.
SOURCE      Escherichia coli
  ORGANISM  Escherichia coli
            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
            Enterobacteriaceae; Escherichia.
REFERENCE   1  (bases 1 to 202)
  AUTHORS   Heruman,B. and Deietoritsuhi,S.
  TITLE     NOVEL DEVELOPMENT REGULATING ARRANGEMENT
  JOURNAL   Patent: JP 1986181386-A 1 14-AUG-1986;
            F HOFFMANN LA ROCHE & CO AG
COMMENT     OS   Escherichia coli
            PN   JP 1986181386-A/1
            PD   14-AUG-1986
            PF   16-DEC-1985 JP 1985282699
            PR   17-DEC-1984 GB 84   8431818
            PI   HERUMAN BUYARUDO, DEIETORITSUHI SUTEYUUBAA
            PC   C12N15/00,C12N1/20,C12N9/10,C12P21/02,(C12N1/20,C12R1:19), PC
             (C12N1/20,
            PC
            C12R1:125),(C12N9/10,C12R1:19),(C12N9/10,C12R1:125),(C12P21/02, PC
             C12R1:19),
            PC   (C12P21/02,C12R1:125);
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
```

```
            CC   anti-sense: No;
            CC   *source: strain=M15;
            FH   Key             Location/Qualifiers
            FH
            FT   promoter        1. .<173
            FT                   /note='P25 promoter'
            FT   sig_peptide     174. .>190
            FT                   /note='lac operator'.
FEATURES             Location/Qualifiers
     source          1. .202
                     /organism="Escherichia coli"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:562"
ORIGIN

  Query Match             100.0%;  Score 51;  DB 6;  Length 202;
  Best Local Similarity   100.0%;  Pred. No. 0.0068;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 174


RESULT 6
A10375
LOCUS       A10375                   207 bp    DNA     linear   PAT 22-SEP-1993
DEFINITION  Nucleotide sequence 22 from patent number EP0303925.
ACCESSION   A10375
VERSION     A10375.1  GI:490697
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 207)
  AUTHORS   Bujard,H. and Lanzer,M.
  TITLE     High repressible sequence for control of expression
  JOURNAL   Patent: EP 0303925-A 22 22-FEB-1989;
            F. HOFFMANN-LA ROCHE AG
FEATURES             Location/Qualifiers
     source          1. .207
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             100.0%;  Score 51;  DB 6;  Length 207;
  Best Local Similarity   100.0%;  Pred. No. 0.0068;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 174


RESULT 7
A11242
LOCUS       A11242                   247 bp    DNA     linear   PAT 12-NOV-1993
DEFINITION  vector pDS1/PN25 XhoI-fragment carrying promoter Pn25 is diplayed.
ACCESSION   A11242
VERSION     A11242.1  GI:491016
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 247)
  AUTHORS   Bujard,H. and Stueber,D.
  TITLE     New expression control sequence
  JOURNAL   Patent: EP 0186069-A 6 02-JUL-1986;
            F. HOFFMANN-LA ROCHE AG
FEATURES             Location/Qualifiers
     source          1. .247
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             100.0%;  Score 51;  DB 6;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 0.0065;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 174


RESULT 8
A10373
LOCUS       A10373                   259 bp    DNA     linear   PAT 22-SEP-1993
DEFINITION  Nucleotide sequence 20 from patent number EP0303925.
ACCESSION   A10373
VERSION     A10373.1  GI:490695
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 259)
  AUTHORS   Bujard,H. and Lanzer,M.
  TITLE     High repressible sequence for control of expression
  JOURNAL   Patent: EP 0303925-A 20 22-FEB-1989;
            F. HOFFMANN-LA ROCHE AG
FEATURES             Location/Qualifiers
     source          1. .259
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             100.0%;  Score 51;  DB 6;  Length 259;
  Best Local Similarity   100.0%;  Pred. No. 0.0064;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 180


RESULT 9
A02739
LOCUS       A02739                  1113 bp    DNA     linear   PAT 23-MAR-1993
DEFINITION  Artificial sequence of plasmid pDS5/RBSII,3A+5A (XhoI/XbaI
            fragment).
ACCESSION   A02739
VERSION     A02739.1  GI:345272
KEYWORDS    chloramphenicol acetyltransferase.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 1113)
  AUTHORS   Gentz,R., Le Grice,S., Mous,J. and Stueber,D.
  TITLE     ENV/GAG polypeptides
  JOURNAL   Patent: EP 0270114-A 5 08-JUN-1988;
            F. HOFFMANN-LA ROCHE AG
FEATURES             Location/Qualifiers
     source          1. .1113
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
     CDS             225. .947
                     /codon_start=1
                     /transl_table=11
                     /product="chloramphenicol acetyltransferase"
                     /protein_id="CAA00265.1"
                     /db_xref="GI:345273"
                     /db_xref="REMTREMBL:CAA00265"
                     /translation="MRGSVDLQPSLARFSGAKEAKMEKKITGYTTVDISQWHRKEHFE
```

AFQSVAQCTYNQTVQLDITAFLKTVKKNKHKFYPAFIHILARLMNAHPEFRMAMKDGE
LVIWDSVHPCYTVFHEQTETFSSLWSEYHDDFRQFLHIYSQDVACYGENLAYFPKGFI
ENMFFVSANPWVSFTSFDLNVANMDNFFAPVFTMGKYYTQGDKVLMPLAIQVHHAVCD
GFHVGRMLNELQQYCDEWQGGA"

ORIGIN

Query Match 100.0%; Score 51; DB 6; Length 1113;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 125 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 175

RESULT 10
A14592
LOCUS A14592 1113 bp DNA circular PAT 21-FEB-1994
DEFINITION Synthetic nucleotide sequence encoding chloramphenicol acetyltransferase (plus 21 additional N-terminus amino acids).
ACCESSION A14592
VERSION A14592.1 GI:491830
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 1113)
AUTHORS Bannwarth,W., Certa,U., Mous,J. and Stueber,D.
TITLE Polypeptides that elicit antibodies against AIDS virus
JOURNAL Patent: EP 0219106-A 5 22-APR-1987;
F. HOFFMANN-LA ROCHE AG
FEATURES Location/Qualifiers
source 1. .1113
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
CDS 225. .947
/codon_start=1
/transl_table=11
/product="chloramphenicol acetyltransferase"
/protein_id="CAA01171.1"
/db_xref="GI:491831"
/db_xref="REMTREMBL:CAA01171"
/translation="MRGSVDLQPSLARFSGAKEAKMEKKITGYTTVDISQWHRKEHFE
AFQSVAQCTYNQTVQLDITAFLKTVKKNKHKFYPAFIHILARLMNAHPEFRMAMKDGE
LVIWDSVHPCYTVFHEQTETFSSLWSEYHDDFRQFLHIYSQDVACYGENLAYFPKGFI
ENMFFVSANPWVSFTSFDLNVANMDNFFAPVFTMGKYYTQGDKVLMPLAIQVHHAVCD
GFHVGRMLNELQQYCDEWQGGA"

ORIGIN

Query Match 100.0%; Score 51; DB 6; Length 1113;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 125 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 175

RESULT 11
A02296
LOCUS A02296 1221 bp DNA linear PAT 18-MAY-1993
DEFINITION Plasmid pDS6/RBSII,3A+5A DNA XhoI/XbaI-fragment.
ACCESSION A02296
VERSION A02296.1 GI:345259
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 1221)
AUTHORS Certa,U., Gentz,R. and Takacs,B.
TITLE Plasmodium falciparum merozoite antigen peptides
JOURNAL Patent: EP 0283829-A 17 28-SEP-1988;
F. HOFFMANN-LA ROCHE AG
FEATURES Location/Qualifiers
source 1. .1221
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 100.0%; Score 51; DB 6; Length 1221;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 125 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 175

RESULT 12
A14593
LOCUS A14593 1221 bp DNA circular PAT 21-FEB-1994
DEFINITION Synthetic nucleotide sequence of the XhoI/XbaI fragment of pDS6/RBSII,3A+5A.
ACCESSION A14593
VERSION A14593.1 GI:491832
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 1221)
AUTHORS Bannwarth,W., Certa,U., Mous,J. and Stueber,D.
TITLE Polypeptides that elicit antibodies against AIDS virus
JOURNAL Patent: EP 0219106-A 6 22-APR-1987;
F. HOFFMANN-LA ROCHE AG
FEATURES Location/Qualifiers
source 1. .1221
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
gene 225. .269
/gene="cat"
CDS 225. .269
/gene="cat"
/codon_start=1
/transl_table=11
/protein_id="CAA01172.1"
/db_xref="GI:491833"
/db_xref="REMTREMBL:CAA01172"
/translation="MRGSVDLQPSLDSC"

ORIGIN

Query Match 100.0%; Score 51; DB 6; Length 1221;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 125 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 175

RESULT 13
A02227
LOCUS A02227 1866 bp DNA linear PAT 29-APR-1996
DEFINITION Plasmid pDS8/RBSII,SphI DNA for XhoI/XbaI fragment.
ACCESSION A02227
VERSION A02227.1 GI:490286
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 1866)
AUTHORS Doebeli,H., Eggimann,B., Gentz,R., Hochuli,E. and Stueber,D.
TITLE Fusion proteins and their purification
JOURNAL Patent: EP 0282042-A 1 14-SEP-1988;

```
           F. HOFFMANN-LA ROCHE AG
FEATURES             Location/Qualifiers
     source          1. .1866
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             100.0%;  Score 51;  DB 6;  Length 1866;
  Best Local Similarity   100.0%;  Pred. No. 0.0042;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 175


RESULT 14
A02295
LOCUS       A02295                  1866 bp    DNA     linear   PAT 18-MAY-1993
DEFINITION  Plasmid pDS8/RBSII,SphI DNA XhoI/XbaI-fragment.
ACCESSION   A02295
VERSION     A02295.1  GI:345258
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 1866)
  AUTHORS   Certa,U., Gentz,R. and Takacs,B.
  TITLE     Plasmodium falciparum merozoite antigen peptides
  JOURNAL   Patent: EP 0283829-A 16 28-SEP-1988;
            F. HOFFMANN-LA ROCHE AG
FEATURES             Location/Qualifiers
     source          1. .1866
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             100.0%;  Score 51;  DB 6;  Length 1866;
  Best Local Similarity   100.0%;  Pred. No. 0.0042;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 175


RESULT 15
A02740
LOCUS       A02740                  1866 bp    DNA     linear   PAT 23-MAR-1993
DEFINITION  Artificial sequence of pDS8/RBSII plasmid (XhoI/XbaI fragment).
ACCESSION   A02740
VERSION     A02740.1  GI:345274
KEYWORDS    dihydrofolate reductase.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 1866)
  AUTHORS   Gentz,R., Le Grice,S., Mous,J. and Stueber,D.
  TITLE     ENV/GAG polypeptides
  JOURNAL   Patent: EP 0270114-A 6 08-JUN-1988;
            F. HOFFMANN-LA ROCHE AG
FEATURES             Location/Qualifiers
     source          1. .1866
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
     CDS             225. .806
                     /codon_start=1
                     /transl_table=11
                     /product="dihydrofolatreductase"
                     /protein_id="CAA00266.1"
                     /db_xref="GI:345275"
                     /db_xref="REMTREMBL:CAA00266"
                     /translation="MRGSGIMVRPLNCIVAVSQNMGIGKNGDLPWPPLRNEFKYFQRM
                     TTTSSVEGKQNLVIMGRKTWFSIPEKNRPLKDRINIVLSRELKEPPRGAHFLAKSLDD
                     ALRLIEQPELASKVDMVWIVGGSSVYQEAMNQPGHLRLFVTRIMQEFESDTFFPEIDL
                     GKYKLLPEYPGVLSEVQEEKGIKYKFEVYEKKD"
ORIGIN

  Query Match             100.0%;  Score 51;  DB 6;  Length 1866;
  Best Local Similarity   100.0%;  Pred. No. 0.0042;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 175


Search completed: April  7, 2004, 04:52:05
Job time : 1683 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 7, 2004, 02:08:25 ; Search time 244 Seconds
(without alignments)
887.943 Million cell updates/sec

Title: US-10-032-393-36
Perfect score: 51
Sequence: 1 tcataaaaaatttatttgct.....ttttctgtataatagattca 51

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	51	100.0	51	6	ABK98620	Abk98620 Gram posi
	2	51	100.0	51	8	ACD13871	Acd13871 Xyl-T5 pr
	3	51	100.0	60	1	AAN70573	Aan70573 Coliphage
	4	51	100.0	72	4	AAH74868	Aah74868 Oligonucl
c	5	51	100.0	80	4	AAH74869	Aah74869 Oligonucl
	6	51	100.0	80	6	ABK98610	Abk98610 Gram posi
	7	51	100.0	80	8	ACD13861	Acd13861 Xyl-T5 fu
	8	51	100.0	94	6	ABK98589	Abk98589 XylO-T5 f
	9	51	100.0	94	8	ACD13840	Acd13840 Oligonucl
c	10	51	100.0	95	6	ABK98590	Abk98590 XylO-T5 f
c	11	51	100.0	95	8	ACD13841	Acd13841 Oligonucl
	12	51	100.0	200	1	AAN91066	Aan91066 Control s
	13	51	100.0	202	1	AAN60262	Aan60262 Plasmid p
	14	51	100.0	207	1	AAN91067	Aan91067 Control s
	15	51	100.0	247	1	AAN60259	Aan60259 Coliphage
	16	51	100.0	259	1	AAN91065	Aan91065 Control s
	17	51	100.0	556	6	ABK98585	Abk98585 Gram posi
	18	51	100.0	556	8	ACD13836	Acd13836 Xyl-T5 fu
	19	51	100.0	1113	1	AAN80481	Aan80481 XhoI/XbaI
	20	51	100.0	1221	1	AAN81153	Aan81153 XhoI/XbaI
	21	51	100.0	1866	1	AAN80482	Aan80482 XhoI/XbaI
	22	51	100.0	1866	1	AAN81356	Aan81356 Sequence
	24	51	100.0	1866	1	AAN80955	Aan80955 XhoI-XbaI
	25	51	100.0	3403	1	AAN80956	Aan80956 Plasmid p
	26	51	100.0	5302	3	AAA98012	Aaa98012 Expressio
	27	51	100.0	5767	3	AAA98014	Aaa98014 Expressio
	28	51	100.0	6852	6	ABK98600	Abk98600 Vector pX
	29	51	100.0	6852	8	ACD13851	Acd13851 Xyl opera
	30	50	98.0	1246	4	AAS50517	Aas50517 Staphyloc
	31	46	90.2	77	1	AAN70113	Aan70113 Sequence
	32	43	84.3	51	6	ABK98621	Abk98621 Gram posi
	33	43	84.3	51	8	ACD13872	Acd13872 Xyl-T5 mu
	34	43	84.3	80	6	ABK98611	Abk98611 Gram posi
	35	43	84.3	80	8	ACD13862	Acd13862 Xyl-T5 mu
	36	43	84.3	94	6	ABK98606	Abk98606 Xyl-T5 DD
	37	43	84.3	94	8	ACD13857	Acd13857 Xyl-T5 mu
c	38	43	84.3	95	6	ABK98607	Abk98607 Xyl-T5 DD
	39	43	84.3	6852	6	ABK98637	Abk98637 Vector pX
	40	43	84.3	6852	8	ACD13888	Acd13888 Xyl-T5 mu
	41	42.8	83.9	83	1	AAN81195	Aan81195 Beta-lact
	42	39.4	77.3	80	1	AAN80462	Aan80462 Expressio
	43	39	76.5	68	1	AAN81260	Aan81260 Hybrid pr
	44	36.4	71.4	41	1	AAN90998	Aan90998 Fragments
	45	33.4	65.5	125	2	AAT04945	Aat04945 Fragment

ALIGNMENTS

RESULT 1
ABK98620
ID ABK98620 standard; DNA; 51 BP.
XX
AC ABK98620;
XX
DT 07-AUG-2003 (revised)
DT 21-OCT-2002 (first entry)
XX
DE Gram positive bacteria Xyl-T5 fusion promoter #3.
XX
KW ds; promoter; gram positive bacteria; fusion promoter; T5; CP25; P32;
KW P59; P1P2; PL; xylO; tetO; trpO; malO; lambdacIO; cellular proliferation;
KW antibiotic.
XX
OS Eubacteria.
OS Bacteriophage T5.
OS Synthetic.
XX
PN WO200251982-A2.
XX
PD 04-JUL-2002.
XX
PF 21-DEC-2001; 2001WO-US050250.
XX
PR 27-DEC-2000; 2000US-0259434P.
PR 06-SEP-2001; 2001US-00948993.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Wall D, Gross M;
XX
DR WPI; 2002-575374/61.
XX
PT Isolated nucleic acid comprises bacterial promoters modified to have
PT altered activity in at least one gram-positive organism, e.g. Bacillus
PT anthracis or Clostridium botulinum, useful for regulating gene expression
PT in bacteria.
XX
PS Claim 2; Page 219; 246pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising a fusion
CC promoter comprising at least one promoter that is modified to have
CC altered activity in at least one gram-positive organism, or comprising
CC T5, CP25, P32, P59, P1P2 or PL linked to at least one operator consisting

CC positioned so binding of a repressor to an operator represses
CC transcription from the fusion promoter. Also included are vectors and
CC host cells comprising the fusion promoters, a method of identifying genes
CC involved in cellular proliferation or required for proliferation of a
CC prokaryotic cell using the vector, a method of identifying compounds that
CC inhibit the proliferation of a prokaryotic cell using the vector, a
CC method of identifying a compound that reduces the activity or level of a
CC gene product required for proliferation of a cell using the vector, a
CC compound identified by the methods, a method of inhibiting the activity
CC or expression of a gene in an operon required for proliferation using the
CC vector, manufacturing an antibiotic comprising using the vector or cell
CC and identifying a nucleic acid with promoter activity in Enterococcus
CC faecalis. The fusion promoters are useful for regulating nucleic acid or
CC polypeptide expression, particularly for regulating gene expression in
CC bacteria and for identifying proliferation-required genes or molecules
CC with potential antibiotic activity. The modified promoters are also
CC useful for replacing endogenous promoters to create cells with specific
CC regulatable genes. The present sequence is a fusion promoter sequence of
CC the invention. (Updated on 07-AUG-2003 to correct OS field.)
XX
SQ Sequence 51 BP; 19 A; 5 C; 5 G; 22 T; 0 U; 0 Other;

Query Match 100.0%; Score 51; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51

RESULT 2
ACD13871
ID ACD13871 standard; DNA; 51 BP.
XX
AC ACD13871;
XX
DT 15-AUG-2003 (first entry)
XX
DE Xyl-T5 promoter sequence.
XX
KW Promoter; ds; gram positive bacteria; Staphylococcus aureus;
KW Enterococcus faecalis; operator; xylO; tetO; trpO; malO; lambda-clO;
KW cellular proliferation.
XX
OS Bacteriophage T5.
OS Unidentified.
XX
PN US2003027286-A1.
XX
PD 06-FEB-2003.
XX
PF 21-DEC-2001; 2001US-00032393.
XX
PR 06-SEP-2000; 2000US-0230335P.
PR 27-DEC-2000; 2000US-0259434P.
XX
PA (HASE/) HASELBECK R.
PA (WALL/) WALL D.
PA (GROS/) GROSS M.
XX
PI Haselbeck R, Wall D, Gross M;
XX
DR WPI; 2003-479541/45.
XX
PT New isolated nucleic acid comprising a fusion promoter having at least
PT one promoter that is modified to have altered activity in at least one
PT gram-positive organism, useful for regulating gene expression in
PT bacteria.
XX
PS Claim 2; Page 80; 142pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising a fusion
CC promoter having at least one promoter that is modified to have altered
CC activity in at least one gram-positive organism (e.g. Staphylococcus
CC aureus or Enterococcus faecalis). The promoter is linked to at least one
CC operator selected from xylO, tetO, trpO, malO and lambda-clO, which are
CC positioned such that the binding of at least one repressor to the
CC operator represses transcription from the fusion promoter. Also included
CC are a vector comprising the isolated nucleic acid, a host cell comprising
CC the nucleic acid. The fusion promoter is useful for identifying genes
CC involved in cellular proliferation, identifying a compound that reduces
CC the activity or level of a gene product required for proliferation of a
CC cell, inhibiting the activity or expression of a gene in an operon
CC required for proliferation, manufacturing an antibiotic, identifying a
CC gene that is required for proliferation of a prokaryotic cell,
CC identifying a compound that inhibits the proliferation of a prokaryotic
CC cell and regulating gene expression in bacteria. The present sequence is
CC a bacterial promoter suitable for inclusion in a fusion promoter of the
CC invention
XX
SQ Sequence 51 BP; 19 A; 5 C; 5 G; 22 T; 0 U; 0 Other;

Query Match 100.0%; Score 51; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51

RESULT 3
AAN70573
ID AAN70573 standard; DNA; 60 BP.
XX
AC AAN70573;
XX
DT 25-MAR-2003 (revised)
DT 11-MAR-1991 (first entry)
XX
DE Coliphage T5 promoter of Bacillus subtilis expression vector.
XX
KW Expression vector; dihydrofolate reductase; IL-2; insulin; HTLV-III; tPA;
KW human renin; ds.
XX
OS Coliphage T5.
XX
FH Key Location/Qualifiers
FT -35_signal 16. .21
FT /*tag= a
FT -10_signal 39. .44
FT /*tag= b
XX
PN EP207459-A.
XX
PD 07-JAN-1987.
XX
PF 27-JUN-1986; 86EP-00108774.
XX
PR 05-JUL-1985; 85GB-00017071.
XX
PA (HOFF) HOFFMANN-LA ROCHE AG.
XX
PI Bujard H, Legrice S;
XX
DR WPI; 1987-001183/01.
XX
PT New gram positive expression control DNA sequences - useful for potent
PT and versatile gene expression of prokaryotic or eukaryotic proteins in
PT bacillus subtilis etc.
XX
PS Disclosure; Table I; 53pp; English.
XX
CC The gene fragment may be incorporated into a novel expression vector, for

CC Bacillus subtilis. Proteins which may be encoded include: dihydrofolate
CC reductase; chloramphenicol acetyltransferase; malaria surface antigens;
CC IL-2; interferons; insulin; tPA; human renin and HTLV-III. (Updated on 25
CC -MAR-2003 to correct PI field.)
XX
SQ Sequence 60 BP; 23 A; 5 C; 6 G; 26 T; 0 U; 0 Other;

Query Match 100.0%; Score 51; DB 1; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51

RESULT 4
AAH74868
ID AAH74868 standard; DNA; 72 BP.
XX
AC AAH74868;
XX
DT 29-OCT-2001 (first entry)
XX
DE Oligonucleotide used to create T5 promoter.
XX
KW Recombinase; genetic engineering; monogenic disorder; ADA deficiency;
KW cystic fibrosis; familial-hypercholesterolaemia; haemophilia;
KW chronic granulomatous disease; Duchenne's muscular dystrophy;
KW Fanconi's disease; anemia; sickle-cell anemia; Gaucher's disease;
KW Hunter's syndrome; X-linked severe combined immunodeficiency; SCID;
KW infectious disease; acquired disorder; tumour; cancer; T5 promoter; ss.
XX
OS Synthetic.
XX
PN WO200161049-A1.
XX
PD 23-AUG-2001.
XX
PF 16-FEB-2001; 2001WO-US005269.
XX
PR 18-FEB-2000; 2000US-0183759P.
XX
PA (STRD) UNIV LELAND STANFORD JUNIOR.
XX
PI Calos MP, Sclimenti CR;
XX
DR WPI; 2001-522610/57.
XX
PT Identifying altered recombinase, involves hybridizing recombination sites
PT in cells having specific coding sequence, transformed with altered
PT recombinase gene, and isolating cells having product of the sequence.
XX
PS Disclosure; Page 59; 101pp; English.
XX
CC The specification describes a method for identifying altered
CC recombinases. The method comprises transforming cells with a first
CC plasmid comprising two recombination sites and a coding sequence of
CC interest, and a second plasmid encoding an altered recombinase; allowing
CC recombination of the two recombination sites using the altered
CC recombinase; screening and isolating transformed cells comprising the
CC product of the sequence of interest; and identifying the altered
CC recombinase. The altered recombinase is useful for site-specifically
CC integrating a polynucleotide sequence of interest in a genome of a cell.
CC It is also useful in genetic engineering of chromosomes of higher cells,
CC and for the generation of transgenic cells, tissues, plants and animals.
CC The altered recombinase is useful for treating monogenic disorders, e.g.
CC ADA deficiency, cystic fibrosis, familial-hypercholesterolaemia, anemia,
CC chronic granulomatous disease, Duchenne's muscular dystrophy,
CC haemophilia, Fanconi's disease, sickle-cell anemia, Gaucher's disease,
CC Hunter's syndrome and X-linked severe combined immunodeficiency (SCID),
CC infectious diseases including viral and bacterial infections, acquired
CC disorders including solid tumours and haematopoietic cancers such as
CC leukaemias and lymphomas, and other cancers. Oligonucleotides AAH74868-69
CC were used to create the T5 promoter, which was used to construct a
CC plasmid for use in the course of the invention
XX
SQ Sequence 72 BP; 27 A; 6 C; 11 G; 28 T; 0 U; 0 Other;

Query Match 100.0%; Score 51; DB 4; Length 72;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 2 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 52

RESULT 5
AAH74869/c
ID AAH74869 standard; DNA; 80 BP.
XX
AC AAH74869;
XX
DT 29-OCT-2001 (first entry)
XX
DE Oligonucleotide used to create T5 promoter.
XX
KW Recombinase; genetic engineering; monogenic disorder; ADA deficiency;
KW cystic fibrosis; familial-hypercholesterolaemia; haemophilia;
KW chronic granulomatous disease; Duchenne's muscular dystrophy;
KW Fanconi's disease; anemia; sickle-cell anemia; Gaucher's disease;
KW Hunter's syndrome; X-linked severe combined immunodeficiency; SCID;
KW infectious disease; acquired disorder; tumour; cancer; T5 promoter; ss.
XX
OS Synthetic.
XX
PN WO200161049-A1.
XX
PD 23-AUG-2001.
XX
PF 16-FEB-2001; 2001WO-US005269.
XX
PR 18-FEB-2000; 2000US-0183759P.
XX
PA (STRD) UNIV LELAND STANFORD JUNIOR.
XX
PI Calos MP, Sclimenti CR;
XX
DR WPI; 2001-522610/57.
XX
PT Identifying altered recombinase, involves hybridizing recombination sites
PT in cells having specific coding sequence, transformed with altered
PT recombinase gene, and isolating cells having product of the sequence.
XX
PS Disclosure; Page 59; 101pp; English.
XX
CC The specification describes a method for identifying altered
CC recombinases. The method comprises transforming cells with a first
CC plasmid comprising two recombination sites and a coding sequence of
CC interest, and a second plasmid encoding an altered recombinase; allowing
CC recombination of the two recombination sites using the altered
CC recombinase; screening and isolating transformed cells comprising the
CC product of the sequence of interest; and identifying the altered
CC recombinase. The altered recombinase is useful for site-specifically
CC integrating a polynucleotide sequence of interest in a genome of a cell.
CC It is also useful in genetic engineering of chromosomes of higher cells,
CC and for the generation of transgenic cells, tissues, plants and animals.
CC The altered recombinase is useful for treating monogenic disorders, e.g.
CC ADA deficiency, cystic fibrosis, familial-hypercholesterolaemia, anemia,
CC chronic granulomatous disease, Duchenne's muscular dystrophy,
CC haemophilia, Fanconi's disease, sickle-cell anemia, Gaucher's disease,
CC Hunter's syndrome and X-linked severe combined immunodeficiency (SCID),
CC infectious diseases including viral and bacterial infections, acquired
CC disorders including solid tumours and haematopoietic cancers such as
CC leukaemias and lymphomas, and other cancers. Oligonucleotides AAH74868-69

CC were used to create the T5 promoter, which was used to construct a
CC plasmid for use in the course of the invention
XX
SQ Sequence 80 BP; 29 A; 14 C; 9 G; 28 T; 0 U; 0 Other;

Query Match 100.0%; Score 51; DB 4; Length 80;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 75 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 25

RESULT 6
ABK98610
ID ABK98610 standard; DNA; 80 BP.
XX
AC ABK98610;
XX
DT 07-AUG-2003 (revised)
DT 21-OCT-2002 (first entry)
XX
DE Gram positive bacteria Xyl-T5 fusion promoter #2.
XX
KW ds; promoter; gram positive bacteria; fusion promoter; T5; CP25; P32;
KW P59; P1P2; PL; xylO; tetO; trpO; malO; lambdaclO; cellular proliferation;
KW antibiotic.
XX
OS Eubacteria.
OS Bacteriophage T5.
OS Synthetic.
XX
PN WO200251982-A2.
XX
PD 04-JUL-2002.
XX
PF 21-DEC-2001; 2001WO-US050250.
XX
PR 27-DEC-2000; 2000US-0259434P.
PR 06-SEP-2001; 2001US-00948993.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Wall D, Gross M;
XX
DR WPI; 2002-575374/61.
XX
PT Isolated nucleic acid comprises bacterial promoters modified to have
PT altered activity in at least one gram-positive organism, e.g. Bacillus
PT anthracis or Clostridium botulinum, useful for regulating gene expression
PT in bacteria.
XX
PS Claim 24; Page 217; 246pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising a fusion
CC promoter comprising at least one promoter that is modified to have
CC altered activity in at least one gram-positive organism, or comprising
CC T5, CP25, P32, P59, P1P2 or PL linked to at least one operator consisting
CC of xylO, tetO, trpO, malO or lambdaclO, where at least one operator is
CC positioned so binding of a repressor to an operator represses
CC transcription from the fusion promoter. Also included are vectors and
CC host cells comprising the fusion promoters, a method of identifying genes
CC involved in cellular proliferation or required for proliferation of a
CC prokaryotic cell using the vector, a method of identifying compounds that
CC inhibit the proliferation of a prokaryotic cell using the vector, a
CC method of identifying a compound that reduces the activity or level of a
CC gene product required for proliferation of a cell using the vector, a
CC compound identified by the methods, a method of inhibiting the activity
CC or expression of a gene in an operon required for proliferation using the
CC vector, manufacturing an antibiotic comprising using the vector or cell
CC and identifying a nucleic acid with promoter activity in Enterococcus
CC faecalis. The fusion promoters are useful for regulating nucleic acid or
CC polypeptide expression, particularly for regulating gene expression in
CC bacteria and for identifying proliferation-required genes or molecules
CC with potential antibiotic activity. The modified promoters are also
CC useful for replacing endogenous promoters to create cells with specific
CC regulatable genes. The present sequence is a fusion promoter sequence of
CC the invention. (Updated on 07-AUG-2003 to correct OS field.)
XX
SQ Sequence 80 BP; 29 A; 8 C; 8 G; 35 T; 0 U; 0 Other;

Query Match 100.0%; Score 51; DB 6; Length 80;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51

RESULT 7
ACD13861
ID ACD13861 standard; DNA; 80 BP.
XX
AC ACD13861;
XX
DT 15-AUG-2003 (first entry)
XX
DE Xyl-T5 fusion promoter #1.
XX
KW Promoter; ds; gram positive bacteria; Staphylococcus aureus;
KW Enterococcus faecalis; operator; xylO; tetO; trpO; malO; lambda-clO;
KW cellular proliferation.
XX
OS Bacteriophage T5.
OS Unidentified.
XX
PN US2003027286-A1.
XX
PD 06-FEB-2003.
XX
PF 21-DEC-2001; 2001US-00032393.
XX
PR 06-SEP-2000; 2000US-0230335P.
PR 27-DEC-2000; 2000US-0259434P.
XX
PA (HASE/) HASELBECK R.
PA (WALL/) WALL D.
PA (GROS/) GROSS M.
XX
PI Haselbeck R, Wall D, Gross M;
XX
DR WPI; 2003-479541/45.
XX
PT New isolated nucleic acid comprising a fusion promoter having at least
PT one promoter that is modified to have altered activity in at least one
PT gram-positive organism, useful for regulating gene expression in
PT bacteria.
XX
PS Claim 24; Page 78; 142pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising a fusion
CC promoter having at least one promoter that is modified to have altered
CC activity in at least one gram-positive organism (e.g. Staphylococcus
CC aureus or Enterococcus faecalis). The promoter is linked to at least one
CC operator selected from xylO, tetO, trpO, malO and lambda-clO, which are
CC positioned such that the binding of at least one repressor to the
CC operator represses transcription from the fusion promoter. Also included
CC are a vector comprising the isolated nucleic acid, a host cell comprising
CC the nucleic acid. The fusion promoter is useful for identifying genes
CC involved in cellular proliferation, identifying a compound that reduces
CC the activity or level of a gene product required for proliferation of a
CC cell, inhibiting the activity or expression of a gene in an operon
CC required for proliferation, manufacturing an antibiotic, identifying a
CC gene that is required for proliferation of a prokaryotic cell,

CC identifying a compound that inhibits the proliferation of a prokaryotic
CC cell and regulating gene expression in bacteria. The present sequence is
CC a fusion promoter of the invention
XX
SQ Sequence 80 BP; 29 A; 8 C; 8 G; 35 T; 0 U; 0 Other;

Query Match 100.0%; Score 51; DB 8; Length 80;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51

RESULT 8
ABK98589
ID ABK98589 standard; DNA; 94 BP.
XX
AC ABK98589;
XX
DT 07-AUG-2003 (revised)
DT 21-OCT-2002 (first entry)
XX
DE Xylo-T5 fusion promoter oligonucleotide #1.
XX
KW ss; promoter; gram positive bacteria; fusion promoter; T5; CP25; P32;
KW P59; P1P2; PL; xylO; tetO; trpO; malO; lambdaclO; cellular proliferation;
KW antibiotic.
XX
OS Eubacteria.
OS Bacteriophage T5.
OS Synthetic.
XX
PN WO200251982-A2.
XX
PD 04-JUL-2002.
XX
PF 21-DEC-2001; 2001WO-US050250.
XX
PR 27-DEC-2000; 2000US-0259434P.
PR 06-SEP-2001; 2001US-00948993.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Wall D, Gross M;
XX
DR WPI; 2002-575374/61.
XX
PT Isolated nucleic acid comprises bacterial promoters modified to have
PT altered activity in at least one gram-positive organism, e.g. Bacillus
PT anthracis or Clostridium botulinum, useful for regulating gene expression
PT in bacteria.
XX
PS Example 1; Page 81; 246pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising a fusion
CC promoter comprising at least one promoter that is modified to have
CC altered activity in at least one gram-positive organism, or comprising
CC T5, CP25, P32, P59, P1P2 or PL linked to at least one operator consisting
CC of xylO, tetO, trpO, malO or lambdaclO, where at least one operator is
CC positioned so binding of a repressor to an operator represses
CC transcription from the fusion promoter. Also included are vectors and
CC host cells comprising the fusion promoters, a method of identifying genes
CC involved in cellular proliferation or required for proliferation of a
CC prokaryotic cell using the vector, a method of identifying compounds that
CC inhibit the proliferation of a prokaryotic cell using the vector, a
CC method of identifying a compound that reduces the activity or level of a
CC gene product required for proliferation of a cell using the vector, a
CC compound identified by the methods, a method of inhibiting the activity
CC or expression of a gene in an operon required for proliferation using the
CC vector, manufacturing an antibiotic comprising using the vector or cell
CC and identifying a nucleic acid with promoter activity in Enterococcus
CC faecalis. The fusion promoters are useful for regulating nucleic acid or
CC polypeptide expression, particularly for regulating gene expression in
CC bacteria and for identifying proliferation-required genes or molecules
CC with potential antibiotic activity. The modified promoters are also
CC useful for replacing endogenous promoters to create cells with specific
CC regulatable genes. The present sequence is an oligonucleotide used to
CC construct a fusion promoter sequence of the invention. (Updated on 07-AUG
CC -2003 to correct OS field.)
XX
SQ Sequence 94 BP; 35 A; 10 C; 12 G; 37 T; 0 U; 0 Other;

Query Match 100.0%; Score 51; DB 6; Length 94;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 6 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 56

RESULT 9
ACD13840
ID ACD13840 standard; DNA; 94 BP.
XX
AC ACD13840;
XX
DT 15-AUG-2003 (first entry)
XX
DE Oligonucleotide Xyl-T5.
XX
KW Promoter; ss; gram positive bacteria; Staphylococcus aureus;
KW Enterococcus faecalis; operator; xylO; tetO; trpO; malO; lambda-clO;
KW cellular proliferation.
XX
OS Escherichia coli.
OS Synthetic.
OS Unidentified.
XX
PN US2003027286-A1.
XX
PD 06-FEB-2003.
XX
PF 21-DEC-2001; 2001US-00032393.
XX
PR 06-SEP-2000; 2000US-0230335P.
PR 27-DEC-2000; 2000US-0259434P.
XX
PA (HASE/) HASELBECK R.
PA (WALL/) WALL D.
PA (GROS/) GROSS M.
XX
PI Haselbeck R, Wall D, Gross M;
XX
DR WPI; 2003-479541/45.
XX
PT New isolated nucleic acid comprising a fusion promoter having at least
PT one promoter that is modified to have altered activity in at least one
PT gram-positive organism, useful for regulating gene expression in
PT bacteria.
XX
PS Example 1; Page 28; 142pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising a fusion
CC promoter having at least one promoter that is modified to have altered
CC activity in at least one gram-positive organism (e.g. Staphylococcus
CC aureus or Enterococcus faecalis). The promoter is linked to at least one
CC operator selected from xylO, tetO, trpO, malO and lambda-clO, which are
CC positioned such that the binding of at least one repressor to the
CC operator represses transcription from the fusion promoter. Also included
CC are a vector comprising the isolated nucleic acid, a host cell comprising
CC the nucleic acid. The fusion promoter is useful for identifying genes
CC involved in cellular proliferation, identifying a compound that reduces
CC the activity or level of a gene product required for proliferation of a

CC cell, inhibiting the activity or expression of a gene in an operon
CC required for proliferation, manufacturing an antibiotic, identifying a
CC gene that is required for proliferation of a prokaryotic cell,
CC identifying a compound that inhibits the proliferation of a prokaryotic
CC cell and regulating gene expression in bacteria. The present sequence is
CC an oligonucleotide used in the construction of a fusion promoter of the
CC invention
XX
SQ Sequence 94 BP; 35 A; 10 C; 12 G; 37 T; 0 U; 0 Other;

Query Match 100.0%; Score 51; DB 8; Length 94;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 6 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 56

RESULT 10
ABK98590/c
ID ABK98590 standard; DNA; 95 BP.
XX
AC ABK98590;
XX
DT 07-AUG-2003 (revised)
DT 21-OCT-2002 (first entry)
XX
DE Xylo-T5 fusion promoter oligonucleotide #2.
XX
KW ss; promoter; gram positive bacteria; fusion promoter; T5; CP25; P32;
KW P59; P1P2; PL; xylO; tetO; trpO; malO; lambdaclO; cellular proliferation;
KW antibiotic.
XX
OS Eubacteria.
OS Bacteriophage T5.
OS Synthetic.
XX
PN WO200251982-A2.
XX
PD 04-JUL-2002.
XX
PF 21-DEC-2001; 2001WO-US050250.
XX
PR 27-DEC-2000; 2000US-0259434P.
PR 06-SEP-2001; 2001US-00948993.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Wall D, Gross M;
XX
DR WPI; 2002-575374/61.
XX
PT Isolated nucleic acid comprises bacterial promoters modified to have
PT altered activity in at least one gram-positive organism, e.g. Bacillus
PT anthracis or Clostridium botulinum, useful for regulating gene expression
PT in bacteria.
XX
PS Example 1; Page 81; 246pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising a fusion
CC promoter comprising at least one promoter that is modified to have
CC altered activity in at least one gram-positive organism, or comprising
CC T5, CP25, P32, P59, P1P2 or PL linked to at least one operator consisting
CC of xylO, tetO, trpO, malO or lambdaclO, where at least one operator is
CC positioned so binding of a repressor to an operator represses
CC transcription from the fusion promoter. Also included are vectors and
CC host cells comprising the fusion promoters, a method of identifying genes
CC involved in cellular proliferation or required for proliferation of a
CC prokaryotic cell using the vector, a method of identifying compounds that
CC inhibit the proliferation of a prokaryotic cell using the vector, a
CC method of identifying a compound that reduces the activity or level of a
CC gene product required for proliferation of a cell using the vector, a
CC compound identified by the methods, a method of inhibiting the activity
CC or expression of a gene in an operon required for proliferation using the
CC vector, manufacturing an antibiotic comprising using the vector or cell
CC and identifying a nucleic acid with promoter activity in Enterococcus
CC faecalis. The fusion promoters are useful for regulating nucleic acid or
CC polypeptide expression, particularly for regulating gene expression in
CC bacteria and for identifying proliferation-required genes or molecules
CC with potential antibiotic activity. The modified promoters are also
CC useful for replacing endogenous promoters to create cells with specific
CC regulatable genes. The present sequence is an oligonucleotide used to
CC construct a fusion promoter sequence of the invention. (Updated on 07-AUG
CC -2003 to correct OS field.)
XX
SQ Sequence 95 BP; 39 A; 11 C; 9 G; 36 T; 0 U; 0 Other;

Query Match 100.0%; Score 51; DB 6; Length 95;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 93 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 43

RESULT 11
ACD13841/c
ID ACD13841 standard; DNA; 95 BP.
XX
AC ACD13841;
XX
DT 15-AUG-2003 (first entry)
XX
DE Oligonucleotide Xyl-T5 complement.
XX
KW Promoter; ss; gram positive bacteria; Staphylococcus aureus;
KW Enterococcus faecalis; operator; xylO; tetO; trpO; malO; lambda-clO;
KW cellular proliferation.
XX
OS Escherichia coli.
OS Synthetic.
OS Unidentified.
XX
PN US2003027286-A1.
XX
PD 06-FEB-2003.
XX
PF 21-DEC-2001; 2001US-00032393.
XX
PR 06-SEP-2000; 2000US-0230335P.
PR 27-DEC-2000; 2000US-0259434P.
XX
PA (HASE/) HASELBECK R.
PA (WALL/) WALL D.
PA (GROS/) GROSS M.
XX
PI Haselbeck R, Wall D, Gross M;
XX
DR WPI; 2003-479541/45.
XX
PT New isolated nucleic acid comprising a fusion promoter having at least
PT one promoter that is modified to have altered activity in at least one
PT gram-positive organism, useful for regulating gene expression in
PT bacteria.
XX
PS Example 1; Page 28; 142pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising a fusion
CC promoter having at least one promoter that is modified to have altered
CC activity in at least one gram-positive organism (e.g. Staphylococcus
CC aureus or Enterococcus faecalis). The promoter is linked to at least one
CC operator selected from xylO, tetO, trpO, malO and lambda-clO, which are
CC positioned such that the binding of at least one repressor to the
CC operator represses transcription from the fusion promoter. Also included

```
CC   are a vector comprising the isolated nucleic acid, a host cell comprising
CC   the nucleic acid. The fusion promoter is useful for identifying genes
CC   involved in cellular proliferation, identifying a compound that reduces
CC   the activity or level of a gene product required for proliferation of a
CC   cell, inhibiting the activity or expression of a gene in an operon
CC   required for proliferation, manufacturing an antibiotic, identifying a
CC   gene that is required for proliferation of a prokaryotic cell,
CC   identifying a compound that inhibits the proliferation of a prokaryotic
CC   cell and regulating gene expression in bacteria. The present sequence is
CC   an oligonucleotide used in the construction of a fusion promoter of the
CC   invention
XX
SQ   Sequence 95 BP; 39 A; 11 C; 9 G; 36 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 51;  DB 8;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-05;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 43


RESULT 12
AAN91066
ID   AAN91066 standard; DNA; 200 BP.
XX
AC   AAN91066;
XX
DT   03-OCT-2002  (revised)
DT   09-JUL-1989  (first entry)
XX
DE   Control sequence N25*/O.
XX
KW   DNA expression control; ss.
XX
OS   Synthetic.
XX
PN   EP303925-A.
XX
PD   22-FEB-1989.
XX
PF   08-AUG-1988;   88EP-00112864.
XX
PR   17-AUG-1987;   87CH-00003152.
XX
PA   (HOFF ) HOFFMANN-LA ROCHE AG.
XX
PI   Bujard H,  Lanzer M;
XX
DR   WPI; 1989-055375/08.
XX
PT   Deoxyribonucleic acid data expression control sequences - comprising
PT   promoter and operator-repressor-sequences.
XX
PS   Disclosure; Fig 7; 65pp; German.
XX
CC   This sequence is the operator N25*/O and is inserted into plasmid pDS3
CC   for expression of a variety of proteins from pro- and eukaryotic sources.
CC   It is prepared as a DNA XhoI/EcoRI frag. This operator/repressor sequence
CC   has a high complexing rate and gives good repressability. See also
CC   N910601-3,5,7,8 and AAN91070. (Updated on 03-OCT-2002 to add missing OS
CC   field.)
XX
SQ   Sequence 200 BP; 64 A; 33 C; 37 G; 66 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 51;  DB 1;  Length 200;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-05;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 174


RESULT 13
AAN60262
ID   AAN60262 standard; DNA; 202 BP.
XX
AC   AAN60262;
XX
DT   29-MAY-1991  (first entry)
XX
DE   Plasmid pDS2/P promoter/operator fusion (PN25x/0).
XX
KW   DHFR; chloramphenicol acetyl-transferase; malaria SA; IL-2; IFN; insulin;
KW   tPA; renin; ds.
XX
OS   Synthetic.
XX
PN   EP186069-A.
XX
PD   02-JUL-1986.
XX
PF   13-DEC-1985;   85EP-00115921.
XX
PR   17-DEC-1984;   84GB-00031818.
XX
PA   (HOFF ) HOFFMANN-LA ROCHE AG.
XX
PI   Bujard H,  Stuber D;
XX
DR   WPI; 1986-170629/27.
XX
PT   Expression control DNA sequence - comprising T5 promoter combined with
PT   DNA sequence which permits control of promoter activity.
XX
PS   Disclosure; Fig 7; 26pp; English.
XX
CC   Plasmid vectors of the pDS1 family may be used to express a sequence
CC   under the control of the colliphage T5 promoter, and one or more
CC   sequences which allow control of the promoter. Sequences expressed
CC   include products such as dihydrofolate reductase; chloramphenicol acetyl-
CC   transferase; malaria surface antigen; IL-2; IFN-alpha, -beta and -gamma;
CC   insulin; growth hormones; tPA; human renin etc
XX
SQ   Sequence 202 BP; 64 A; 34 C; 37 G; 67 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 51;  DB 1;  Length 202;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-05;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 174


RESULT 14
AAN91067
ID   AAN91067 standard; DNA; 207 BP.
XX
AC   AAN91067;
XX
DT   03-OCT-2002  (revised)
DT   09-JUL-1989  (first entry)
XX
DE   Control sequence N25OP29.
XX
KW   DNA expression control; ss.
XX
OS   Synthetic.
XX
PN   EP303925-A.
XX
PD   22-FEB-1989.
XX
```

PF 08-AUG-1988; 88EP-00112864.
XX
PR 17-AUG-1987; 87CH-00003152.
XX
PA (HOFF) HOFFMANN-LA ROCHE AG.
XX
PI Bujard H, Lanzer M;
XX
DR WPI; 1989-055375/08.
XX
PT Deoxyribonucleic acid data expression control sequences - comprising
PT promoter and operator-repressor-sequences.
XX
PS Disclosure; Fig 7; 65pp; German.
XX
CC Sequence is the operator/promoter N25OP29 and is inserted into plasmid
CC pDS3 for expression of a variety of proteins from pro- and eukaryotic
CC sources. It is prepared as a DNA XhoI/EcoRI frag. It comprises a low
CC signal strength/high promoter strength promoter and high complexing rate
CC operator/repressor. It gives high transcription and translation efficienc
CC ies and good repressability. See also AAN91060, 1,2,3,5,6,8 and AAN91070.
CC (Updated on 03-OCT-2002 to add missing OS field.)
XX
SQ Sequence 207 BP; 66 A; 37 C; 37 G; 67 T; 0 U; 0 Other;

Query Match 100.0%; Score 51; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 124 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 174

RESULT 15
AAN60259
ID AAN60259 standard; DNA; 247 BP.
XX
AC AAN60259;
XX
DT 27-AUG-2003 (revised)
DT 29-MAY-1991 (first entry)
XX
DE Coliphage PN25 Pre-early promoter of plasmid pDS1,PN25,to1+.
XX
KW DHFR; chloramphenicol acetyl-transferase; malaria SA; IL-2; IFN; insulin;
KW tPA; renin.
XX
OS Unidentified.
XX
PN EP186069-A.
XX
PD 02-JUL-1986.
XX
PF 13-DEC-1985; 85EP-00115921.
XX
PR 17-DEC-1984; 84GB-00031818.
XX
PA (HOFF) HOFFMANN-LA ROCHE AG.
XX
PI Bujard H, Stuber D;
XX
DR WPI; 1986-170629/27.
XX
PT Expression control DNA sequence - comprising T5 promoter combined with
PT DNA sequence which permits control of promoter activity.
XX
PS Disclosure; Fig 2; 26pp; English.
XX
CC Plasmid vectors of the pDS1 family may be used to express a sequence
CC under the control of a coliphage T5 promoter eg. the coliphage PN25 pre-
CC early promoter, and one or more sequences which allow control of the
CC promoter. Sequences expressed include products such as dihydrofolate
CC reductase; chloramphenicol acetyl-transferase; malaria surface antigen;
CC IL-2; IFN-alpha, -beta and -gamma; insulin; growth hormones; tPA; human
CC renin etc. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 247 BP; 79 A; 44 C; 48 G; 76 T; 0 U; 0 Other;

Query Match 100.0%; Score 51; DB 1; Length 247;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 124 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 174

Search completed: April 7, 2004, 04:23:52
Job time : 246 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 7, 2004, 04:19:50 ; Search time 52 Seconds
(without alignments)
544.279 Million cell updates/sec

Title: US-10-032-393-36
Perfect score: 51
Sequence: 1 tcataaaaaatttatttgct.....ttttctgtataatagattca 51

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	33.4	65.5	125	1	US-08-400-864-2	Sequence 2, Appli
	2	33	64.7	171	2	US-08-892-272-3	Sequence 3, Appli
	3	33	64.7	757	2	US-08-892-272-1	Sequence 1, Appli
	4	31.4	61.6	49	1	US-08-400-864-1	Sequence 1, Appli
	5	28.6	56.1	247	3	US-09-344-888A-24	Sequence 24, Appl
	6	28.6	56.1	250	3	US-08-840-466A-25	Sequence 25, Appl
	7	28.6	56.1	250	4	US-09-696-188B-25	Sequence 25, Appl
	8	28.6	56.1	520	1	US-08-268-348A-7	Sequence 7, Appli
	9	28.6	56.1	520	1	US-08-268-348A-9	Sequence 9, Appli
	10	28.6	56.1	1106	1	US-08-041-648-4	Sequence 4, Appli
	11	28.6	56.1	1106	1	US-08-041-648-6	Sequence 6, Appli
	12	28.6	56.1	1106	1	US-08-041-648-8	Sequence 8, Appli
	13	28.6	56.1	3462	4	US-09-742-373-10	Sequence 10, Appl
	14	28.6	56.1	3977	1	US-07-794-400-2	Sequence 2, Appli
	15	28.6	56.1	3977	1	US-07-794-400-13	Sequence 13, Appl
	16	28.6	56.1	3977	1	US-08-041-648-1	Sequence 1, Appli
	17	28.6	56.1	3977	1	US-08-217-529-1	Sequence 1, Appli
	18	28.6	56.1	3977	1	US-08-397-470-2	Sequence 2, Appli
	19	28.6	56.1	3977	1	US-08-397-470-13	Sequence 13, Appl
	20	28.6	56.1	4202	4	US-09-483-419-2	Sequence 2, Appli
	21	28.6	56.1	4491	4	US-09-837-863-23	Sequence 23, Appl
	22	28.6	56.1	4755	4	US-09-837-863-24	Sequence 24, Appl
	23	28.6	56.1	6501	4	US-09-767-515-1	Sequence 1, Appli
	24	28.6	56.1	6501	4	US-09-767-515-2	Sequence 2, Appli
c	25	27.2	53.3	1830121	4	US-09-557-884-1	Sequence 1, Appli
c	26	27.2	53.3	1830121	4	US-09-643-990A-1	Sequence 1, Appli
c	28	25.4	49.8	843	4	US-09-134-001C-2669	Sequence 2669, Ap
	29	25	49.0	92407	4	US-09-596-002-36	Sequence 36, Appl
	30	25	49.0	640681	4	US-09-790-988-1	Sequence 1, Appli
c	31	24.8	48.6	6152	3	US-08-973-462-1	Sequence 1, Appli
c	32	24.4	47.8	2728	4	US-09-620-312D-572	Sequence 572, App
c	33	24.4	47.8	15788	4	US-09-920-759-13	Sequence 13, Appl
	34	24.4	47.8	193303	4	US-09-497-855A-37	Sequence 37, Appl
	35	24.4	47.8	193303	4	US-09-497-855A-44	Sequence 44, Appl
	36	24.2	47.5	1650	4	US-09-907-794A-254	Sequence 254, App
	37	24.2	47.5	1650	4	US-09-905-125A-254	Sequence 254, App
	38	24.2	47.5	1650	4	US-09-902-775A-254	Sequence 254, App
c	39	24	47.1	640681	4	US-09-790-988-1	Sequence 1, Appli
	40	23.8	46.7	786431	4	US-09-751-389-3	Sequence 3, Appli
	41	23.6	46.3	2243	1	US-07-995-657-1	Sequence 1, Appli
	42	23.6	46.3	2243	1	US-08-474-587-1	Sequence 1, Appli
	43	23.6	46.3	2349	2	US-08-974-546-2	Sequence 2, Appli
	44	23.6	46.3	6113	4	US-10-204-708-14	Sequence 14, Appl
c	45	23.6	46.3	112132	4	US-09-741-150-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-400-864-2
; Sequence 2, Application US/08400864
; Patent No. 5721137
; GENERAL INFORMATION:
; APPLICANT: FRASCOTTI, GIANNI
; APPLICANT: GRANDI, GUIDO
; TITLE OF INVENTION: PLASMID VECTOR AND ITS USE FOR THE
; TITLE OF INVENTION: PRODUCTION OF HETEROLOGOUS PROTEINS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/400,864
; FILING DATE: 08-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IT 000727 MI94A
; FILING DATE: 15-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 2264-083-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 125 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-400-864-2

Query Match 65.5%; Score 33.4; DB 1; Length 125;
Best Local Similarity 95.7%; Pred. No. 0.16;
Matches 45; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

```
Qy          6 AAAAATTTATTTGCTTTCAGGAAAA-TTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||||||||||| ||||| ||||||||||||||||
Db          5 AAAAATTTATTTGCTTTCAGGAAAATTTTTTATGTATAATAGATTCA 51


RESULT 2
US-08-892-272-3
; Sequence 3, Application US/08892272
; Patent No. 5891687
;  GENERAL INFORMATION:
;    APPLICANT:  SCHLIEPER, Daniel
;    APPLICANT:  SOBEK, Harald
;    APPLICANT:  SCHMIDT, Manfred
;    APPLICANT:  VON WILKEN-BERGMANN, Brigitte
;    APPLICANT:  MULLER-HILL, Benno
;    TITLE OF INVENTION:  POSITIVE SELECTION VECTOR BASED ON THE
;    TITLE OF INVENTION:  CAPS GENE, pCAPs VECTOR AND ITS USE
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nikaido, Marmelstein, Murray & Oram
;      STREET:  655 Fifteenth Street N.W. Suite 330
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-5701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/892,272
;      FILING DATE:  14-JUL-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE 196 30 617.5
;      FILING DATE:  29-JUL-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murray, Robert B.
;      REGISTRATION NUMBER:  22,980
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)638-5000
;      TELEFAX:  (202)638-4810
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  171 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-892-272-3

  Query Match             64.7%;  Score 33;  DB 2;  Length 171;
  Best Local Similarity   79.6%;  Pred. No. 0.21;
  Matches   39;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          3 ATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||||||||| | | || |   |||||||   |||
Db         71 ATAAAAAATTTATTTGCTTTCAGGTACAATTCTTGATATAATATTATCA 119


RESULT 3
US-08-892-272-1
; Sequence 1, Application US/08892272
; Patent No. 5891687
;  GENERAL INFORMATION:
;    APPLICANT:  SCHLIEPER, Daniel
;    APPLICANT:  SOBEK, Harald
;    APPLICANT:  SCHMIDT, Manfred
;    APPLICANT:  VON WILKEN-BERGMANN, Brigitte
;    APPLICANT:  MULLER-HILL, Benno
;    TITLE OF INVENTION:  POSITIVE SELECTION VECTOR BASED ON THE
;    TITLE OF INVENTION:  CAPS GENE, pCAPs VECTOR AND ITS USE
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nikaido, Marmelstein, Murray & Oram
;      STREET:  655 Fifteenth Street N.W. Suite 330
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-5701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/892,272
;      FILING DATE:  14-JUL-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE 196 30 617.5
;      FILING DATE:  29-JUL-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murray, Robert B.
;      REGISTRATION NUMBER:  22,980
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)638-5000
;      TELEFAX:  (202)638-4810
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  757 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  90..722
US-08-892-272-1

  Query Match             64.7%;  Score 33;  DB 2;  Length 757;
  Best Local Similarity   79.6%;  Pred. No. 0.22;
  Matches   39;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          3 ATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||||||||| | | || |   |||||||   |||
Db         13 ATAAAAAATTTATTTGCTTTCAGGTACAATTCTTGATATAATATTATCA 61


RESULT 4
US-08-400-864-1
; Sequence 1, Application US/08400864
; Patent No. 5721137
;  GENERAL INFORMATION:
;    APPLICANT:  FRASCOTTI, GIANNI
;    APPLICANT:  GRANDI, GUIDO
;    TITLE OF INVENTION:  PLASMID VECTOR AND ITS USE FOR THE
;    TITLE OF INVENTION:  PRODUCTION OF HETEROLOGOUS PROTEINS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
;      STREET:  1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
;      CITY:  ARLINGTON
;      STATE:  VIRGINIA
;      COUNTRY:  USA
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
```

```
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  IT 000727 MI94A
;      FILING DATE:  15-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OBLON, NORMAN F
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  2264-083-0
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 413-3000
;      TELEFAX:  (703) 413-2220
;      TELEX:  248855 OPAT UR
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  49 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-400-864-1

  Query Match             61.6%;  Score 31.4;  DB 1;  Length 49;
  Best Local Similarity   95.6%;  Pred. No. 0.57;
  Matches   43;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          6 AAAAATTTATTTGCTTTCAGGAAAA-TTTTTCTGTATAATAGATT 49
              ||||||||||||||||||||||||| ||||| |||||||||||||
Db          5 AAAAATTTATTTGCTTTCAGGAAAATTTTTTATGTATAATAGATT 49


RESULT 5
US-09-344-888A-24
; Sequence 24, Application US/09344888A
; Patent No. 6291245
; GENERAL INFORMATION:
;  APPLICANT:  Kopetzki, Erhard
;  APPLICANT:  Schantz, Christian
;  TITLE OF INVENTION:  New Host-Vector System
;  FILE REFERENCE:  CD20315
;  CURRENT APPLICATION NUMBER: US/09/344,888A
;  CURRENT FILING DATE:  1999-06-25
;  PRIOR APPLICATION NUMBER:  EP98113156.8
;  PRIOR FILING DATE:  1998-07-15
;  PRIOR APPLICATION NUMBER:  EP98119078.8
;  PRIOR FILING DATE:  1998-10-09
;  NUMBER OF SEQ ID NOS:  24
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 24
;   LENGTH: 247
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:expression cassette
US-09-344-888A-24

  Query Match             56.1%;  Score 28.6;  DB 3;  Length 247;
  Best Local Similarity   72.5%;  Pred. No. 3.8;
  Matches   37;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||||||||  |      |      ||||||||||||
Db         10 TCATAAAAAATTTATTTGCTTTGTGAGCGGATAACAATTATAATAGATTCA 60


RESULT 6
US-08-840-466A-25
; Sequence 25, Application US/08840466A
; Patent No. 6261561
;   GENERAL INFORMATION:
;       APPLICANT: Stewart, C. Neal
;                  Mckee, Marian L.
;                  O'Brien, Alison D.
;                  Wachtel, Marian R.
;       TITLE OF INVENTION: Method Of Stimulating An Immune Response
;                           By Administration Of Host Organisms That Express Intimin
;                           Alone Or As A Fusion Protein With One Or More Other
;                           Antigens.
;       NUMBER OF SEQUENCES: 27
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
;                       Dunner, L.L.P.
;            STREET: 1300 I Street, N.W., Suite 700
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20005-3315
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/840,466A
;            FILING DATE: 18-Apr-1997
;            CLASSIFICATION: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Boone, Laural S.
;            REGISTRATION NUMBER: 43,505
;            REFERENCE/DOCKET NUMBER: 04995.0029-00000
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202) 408-4000
;            TELEFAX: (202) 408-4400
;  INFORMATION FOR SEQ ID NO: 25:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 250 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;       SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-08-840-466A-25

  Query Match             56.1%;  Score 28.6;  DB 3;  Length 250;
  Best Local Similarity   72.5%;  Pred. No. 3.8;
  Matches   37;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||||||||  |      |      ||||||||||||
Db         10 TCATAAAAAATTTATTTGCTTTGTGAGCGGATAACAATTATAATAGATTCA 60


RESULT 7
US-09-696-188B-25
; Sequence 25, Application US/09696188B
; Patent No. 6406885
;   GENERAL INFORMATION:
;       APPLICANT: Stewart, C. Neal
;                  Mckee, Marian L.
;                  O'Brien, Alison D.
;                  Wachtel, Marian R.
;       TITLE OF INVENTION: Method Of Stimulating An Immune Response
;                           By Administration Of Host Organisms That Express Intimin
;                           Alone Or As A Fusion Protein With One Or More Other
;                           Antigens.
;       NUMBER OF SEQUENCES: 27
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
;                       Dunner, L.L.P.
;            STREET: 1300 I Street, N.W., Suite 700
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20005-3315
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
```

```
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/696,188B
;           FILING DATE: 26-Oct-2000
;           CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: 08/840,466
;           FILING DATE: 1997-04-18
;       ATTORNEY/AGENT INFORMATION:
;           NAME: Boone, Laural S.
;           REGISTRATION NUMBER: 43,505
;           REFERENCE/DOCKET NUMBER: 04995.0029-00000
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (202) 408-4000
;           TELEFAX: (202) 408-4400
;   INFORMATION FOR SEQ ID NO: 25:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 250 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;       SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-696-188B-25

  Query Match             56.1%;  Score 28.6;  DB 4;  Length 250;
  Best Local Similarity   72.5%;  Pred. No. 3.8;
  Matches   37;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||||||| |      |      ||||||||||||
Db         10 TCATAAAAAATTTATTTGCTTTGTGAGCGGATAACAATTATAATAGATTCA 60


RESULT 8
US-08-268-348A-7
; Sequence 7, Application US/08268348A
; Patent No. 5750374
;  GENERAL INFORMATION:
;    APPLICANT:  Dobeli, Heinz
;    APPLICANT:  Draeger, Nicholas
;    APPLICANT:  Trottman, Gerda H
;    APPLICANT:  Jakob, Peter
;    APPLICANT:  Stuber, Dietrich
;    TITLE OF INVENTION:  Process for Producing Hydrophobic
;    TITLE OF INVENTION:  Polypeptides and Proteins, and Fusion Proteins for Use in
;    TITLE OF INVENTION:  Producing Same
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/268,348A
;      FILING DATE:  29-JUN-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 93110755.1
;      FILING DATE:  06-JUL-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Parise, John P.
;      REGISTRATION NUMBER:  34,403
;      REFERENCE/DOCKET NUMBER:  4105/157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-6326
;      TELEFAX:  (201) 235-3500
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  520 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  115..516
;      OTHER INFORMATION:  /product= "Amyloid Protein AA"
US-08-268-348A-7

  Query Match             56.1%;  Score 28.6;  DB 1;  Length 520;
  Best Local Similarity   72.5%;  Pred. No. 4;
  Matches   37;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||||||| |      |      ||||||||||||
Db         10 TCATAAAAAATTTATTTGCTTTGTGAGCGGATAACAATTATAATAGATTCA 60


RESULT 9
US-08-268-348A-9
; Sequence 9, Application US/08268348A
; Patent No. 5750374
;  GENERAL INFORMATION:
;    APPLICANT:  Dobeli, Heinz
;    APPLICANT:  Draeger, Nicholas
;    APPLICANT:  Trottman, Gerda H
;    APPLICANT:  Jakob, Peter
;    APPLICANT:  Stuber, Dietrich
;    TITLE OF INVENTION:  Process for Producing Hydrophobic
;    TITLE OF INVENTION:  Polypeptides and Proteins, and Fusion Proteins for Use in
;    TITLE OF INVENTION:  Producing Same
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/268,348A
;      FILING DATE:  29-JUN-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 93110755.1
;      FILING DATE:  06-JUL-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Parise, John P.
;      REGISTRATION NUMBER:  34,403
;      REFERENCE/DOCKET NUMBER:  4105/157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-6326
;      TELEFAX:  (201) 235-3500
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  520 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  115..516
```

```
;      OTHER INFORMATION:  /product= "Amyloid Protein AA"
US-08-268-348A-9

  Query Match             56.1%;  Score 28.6;  DB 1;  Length 520;
  Best Local Similarity   72.5%;  Pred. No. 4;
  Matches   37;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||||||  |     |     ||||||||||||
Db         10 TCATAAAAAATTTATTTGCTTTGTGAGCGGATAACAATTATAATAGATTCA 60


RESULT 10
US-08-041-648-4
; Sequence 4, Application US/08041648
; Patent No. 5486463
;  GENERAL INFORMATION:
;    APPLICANT:  Lesslauer, Werner
;    APPLICANT:  L tscher, Hansruedi
;    APPLICANT:  St ber, Dietrich
;    TITLE OF INVENTION:  TNF-MUTEINS
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  George M. Gould, Esq., Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07110-1199
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/041,648
;      FILING DATE:  1-APR-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 92810249.0
;      FILING DATE:  2-APR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Roseman, Catherine R.
;      REGISTRATION NUMBER:  34240
;      REFERENCE/DOCKET NUMBER:  RAN 4105/147
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-6208
;      TELEFAX:  (201) 235-3500
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1106 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  Plasmid pDS56/RBSII,SphI-THFalpha(Trp32)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  994..1104
US-08-041-648-4

  Query Match             56.1%;  Score 28.6;  DB 1;  Length 1106;
  Best Local Similarity   72.5%;  Pred. No. 4.1;
  Matches   37;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||||||  |     |     ||||||||||||
Db        886 TCATAAAAAATTTATTTGCTTTGTGAGCGGATAACAATTATAATAGATTCA 936


RESULT 11
US-08-041-648-6
; Sequence 6, Application US/08041648
; Patent No. 5486463
;  GENERAL INFORMATION:
;    APPLICANT:  Lesslauer, Werner
;    APPLICANT:  L tscher, Hansruedi
;    APPLICANT:  St ber, Dietrich
;    TITLE OF INVENTION:  TNF-MUTEINS
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  George M. Gould, Esq., Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07110-1199
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/041,648
;      FILING DATE:  1-APR-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 92810249.0
;      FILING DATE:  2-APR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Roseman, Catherine R.
;      REGISTRATION NUMBER:  34240
;      REFERENCE/DOCKET NUMBER:  RAN 4105/147
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-6208
;      TELEFAX:  (201) 235-3500
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1106 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  Plasmid pDS56/RBSII,SphI-TNFalpha(Ser29)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  994..1104
US-08-041-648-6

  Query Match             56.1%;  Score 28.6;  DB 1;  Length 1106;
  Best Local Similarity   72.5%;  Pred. No. 4.1;
  Matches   37;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||||||  |     |     ||||||||||||
Db        886 TCATAAAAAATTTATTTGCTTTGTGAGCGGATAACAATTATAATAGATTCA 936


RESULT 12
US-08-041-648-8
; Sequence 8, Application US/08041648
; Patent No. 5486463
;  GENERAL INFORMATION:
;    APPLICANT:  Lesslauer, Werner
;    APPLICANT:  L tscher, Hansruedi
;    APPLICANT:  St ber, Dietrich
;    TITLE OF INVENTION:  TNF-MUTEINS
;    NUMBER OF SEQUENCES:  17
```

```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  George M. Gould, Esq., Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  U.S.A.
;      ZIP:  07110-1199
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/041,648
;      FILING DATE:  1-APR-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 92810249.0
;      FILING DATE:  2-APR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Roseman, Catherine R.
;      REGISTRATION NUMBER:  34240
;      REFERENCE/DOCKET NUMBER:  RAN 4105/147
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-6208
;      TELEFAX:  (201) 235-3500
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1106 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  Plasmid pDS56/RBSII,SphI-TNFalpha(Ser29Trp32)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  994..1104
US-08-041-648-8

  Query Match             56.1%;  Score 28.6;  DB 1;  Length 1106;
  Best Local Similarity   72.5%;  Pred. No. 4.1;
  Matches   37;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              ||||||||||||||||||||||| |      |      ||||||||||||||
Db        886 TCATAAAAAATTTATTTGCTTTGTGAGCGGATAACAATTATAATAGATTCA 936


RESULT 13
US-09-742-373-10
; Sequence 10, Application US/09742373
; Patent No. 6562946
; GENERAL INFORMATION:
;  APPLICANT:  Althaus, Harald
;  APPLICANT:  Hauser, Hans-Peter
;  TITLE OF INVENTION:  Human Procalcitonin and the Preparation and Use Thereof
;  FILE REFERENCE:  05552.1445-00
;  CURRENT APPLICATION NUMBER: US/09/742,373
;  CURRENT FILING DATE:  2000-12-22
;  PRIOR APPLICATION NUMBER:  19962434.8
;  PRIOR FILING DATE:  1999-12-22
;  PRIOR APPLICATION NUMBER:  10016278.9
;  PRIOR FILING DATE:  2000-04-03
;  PRIOR APPLICATION NUMBER:  10027954.6
;  PRIOR FILING DATE:  2000-06-08
;  NUMBER OF SEQ ID NOS:  12
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 3462
;   TYPE: DNA
;   ORGANISM: Unknown Organism
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism: Vectorsequence ,
;   OTHER INFORMATION: DNA
US-09-742-373-10

  Query Match             56.1%;  Score 28.6;  DB 4;  Length 3462;
  Best Local Similarity   72.5%;  Pred. No. 4.3;
  Matches   37;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              ||||||||||||||||||||||| |      |      ||||||||||||||
Db         10 TCATAAAAAATTTATTTGCTTTGTGAGCGGATAACAATTATAATAGATTCA 60


RESULT 14
US-07-794-400-2
; Sequence 2, Application US/07794400
; Patent No. 5422104
;  GENERAL INFORMATION:
;    APPLICANT:  Fiers, W.
;    APPLICANT:  Tavernier, J.
;    APPLICANT:  Van Ostade, X.
;    TITLE OF INVENTION:  TNF-Muteins
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/794,400
;      FILING DATE:  19911120
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 90810901.0
;      FILING DATE:  21-NOV-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Krovatin, William
;      REGISTRATION NUMBER:  33256
;      REFERENCE/DOCKET NUMBER:  4105/136-00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4387
;      TELEFAX:  (201) 235-3500
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3977 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (recombinant plasmid)
;    IMMEDIATE SOURCE:
;      CLONE:  pDS56/RBSII,Sph1-TNF-alpha
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  115..591
US-07-794-400-2

  Query Match             56.1%;  Score 28.6;  DB 1;  Length 3977;
  Best Local Similarity   72.5%;  Pred. No. 4.3;
  Matches   37;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              ||||||||||||||||||||||| |      |      ||||||||||||||
Db         10 TCATAAAAAATTTATTTGCTTTGTGAGCGGATAACAATTATAATAGATTCA 60
```

```
RESULT 15
US-07-794-400-13
; Sequence 13, Application US/07794400
; Patent No. 5422104
;  GENERAL INFORMATION:
;    APPLICANT:  Fiers, W.
;    APPLICANT:  Tavernier, J.
;    APPLICANT:  Van Ostade, X.
;    TITLE OF INVENTION:  TNF-Muteins
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/794,400
;      FILING DATE:  19911120
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 90810901.0
;      FILING DATE:  21-NOV-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Krovatin, William
;      REGISTRATION NUMBER:  33256
;      REFERENCE/DOCKET NUMBER:  4105/136-00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4387
;      TELEFAX:  (201) 235-3500
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3977 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (recombinant plasmid)
;    IMMEDIATE SOURCE:
;      CLONE:  pDS56/RBSII,Sph1-TNF-alpha
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  115..591
;    FEATURE:
;      NAME/KEY:  Modified site
;      LOCATION:  202-204, 208-210 and 211-213
;      OTHER INFORMATION:  /note= "N = A, G, C or T"
US-07-794-400-13

  Query Match             56.1%;  Score 28.6;  DB 1;  Length 3977;
  Best Local Similarity   72.5%;  Pred. No. 4.3;
  Matches   37;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||||||  |     |      ||||||||||||
Db         10 TCATAAAAAATTTATTTGCTTTGTGAGCGGATAACAATTATAATAGATTCA 60


Search completed: April  7, 2004, 05:43:46
Job time : 56 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 7, 2004, 04:12:30 ; Search time 1006 Seconds
(without alignments)
189.995 Million cell updates/sec

Title: US-10-032-393-36
Perfect score: 51
Sequence: 1 tcataaaaaatttatttgct.....ttttctgtataatagattca 51

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2470632 seqs, 1873875610 residues

Total number of hits satisfying chosen parameters: 4941264

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	51	100.0	51	14	US-10-032-393-36	Sequence 36, Appl
	2	51	100.0	72	9	US-09-788-297-6	Sequence 6, Appli
c	3	51	100.0	80	9	US-09-788-297-7	Sequence 7, Appli
	4	51	100.0	80	14	US-10-032-393-26	Sequence 26, Appl
	5	51	100.0	94	14	US-10-032-393-5	Sequence 5, Appli
c	6	51	100.0	95	14	US-10-032-393-6	Sequence 6, Appli
	7	51	100.0	556	14	US-10-032-393-1	Sequence 1, Appli
	8	51	100.0	5302	15	US-10-385-415-2	Sequence 2, Appli
	9	51	100.0	5767	15	US-10-385-415-4	Sequence 4, Appli
	10	51	100.0	6852	14	US-10-032-393-16	Sequence 16, Appl
	11	50	98.0	1246	9	US-09-815-242-3094	Sequence 3094, Ap
	12	43	84.3	51	14	US-10-032-393-37	Sequence 37, Appl
	13	43	84.3	80	14	US-10-032-393-27	Sequence 27, Appl
	14	43	84.3	94	14	US-10-032-393-22	Sequence 22, Appl
c	15	43	84.3	95	14	US-10-032-393-23	Sequence 23, Appl
	16	43	84.3	6852	14	US-10-032-393-53	Sequence 53, Appl
	17	29.8	58.4	113515	14	US-10-311-455-2148	Sequence 2148, Ap
	18	28.6	56.1	82	14	US-10-288-858-13	Sequence 13, Appl
	19	28.6	56.1	94	14	US-10-032-393-12	Sequence 12, Appl
c	20	28.6	56.1	95	14	US-10-032-393-13	Sequence 13, Appl
	21	28.6	56.1	134	14	US-10-284-083-3	Sequence 3, Appli
	22	28.6	56.1	138	14	US-10-284-083-4	Sequence 4, Appli
	23	28.6	56.1	138	14	US-10-284-083-5	Sequence 5, Appli
	24	28.6	56.1	162	9	US-09-828-523A-97	Sequence 97, Appl
	25	28.6	56.1	162	10	US-09-966-521-89	Sequence 89, Appl
	26	28.6	56.1	162	14	US-10-429-094-89	Sequence 89, Appl
	27	28.6	56.1	166	14	US-10-284-083-2	Sequence 2, Appli
	28	28.6	56.1	170	14	US-10-284-083-6	Sequence 6, Appli
	29	28.6	56.1	250	8	US-08-837-459-25	Sequence 25, Appl
	30	28.6	56.1	250	14	US-10-150-058-25	Sequence 25, Appl
	31	28.6	56.1	2220	14	US-10-288-858-5	Sequence 5, Appli
	32	28.6	56.1	3420	15	US-10-385-415-1	Sequence 1, Appli
	33	28.6	56.1	3462	9	US-09-742-373-10	Sequence 10, Appl
	34	28.6	56.1	3462	14	US-10-394-058-10	Sequence 10, Appl
	35	28.6	56.1	3876	15	US-10-385-415-27	Sequence 27, Appl
	36	28.6	56.1	3876	15	US-10-385-415-28	Sequence 28, Appl
	37	28.6	56.1	3879	15	US-10-385-415-5	Sequence 5, Appli
	38	28.6	56.1	3879	15	US-10-385-415-6	Sequence 6, Appli
	39	28.6	56.1	3879	15	US-10-385-415-7	Sequence 7, Appli
	40	28.6	56.1	3879	15	US-10-385-415-21	Sequence 21, Appl
	41	28.6	56.1	3879	15	US-10-385-415-25	Sequence 25, Appl
	42	28.6	56.1	3879	15	US-10-385-415-26	Sequence 26, Appl
	43	28.6	56.1	3885	15	US-10-385-415-3	Sequence 3, Appli
	44	28.6	56.1	3897	15	US-10-385-415-20	Sequence 20, Appl
	45	28.6	56.1	3900	15	US-10-385-415-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-10-032-393-36
; Sequence 36, Application US/10032393
; Publication No. US20030027286A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Wall, Daniel
; APPLICANT: Gross, Molly
; TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
; FILE REFERENCE: ELITRA.010A
; CURRENT APPLICATION NUMBER: US/10/032,393
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/259,434
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: 09/948,993
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Xyl-T5 promoter sequence
US-10-032-393-36

Query Match 100.0%; Score 51; DB 14; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51

RESULT 2

```
US-09-788-297-6
; Sequence 6, Application US/09788297
; Patent No. US20020094516A1
; GENERAL INFORMATION:
;  APPLICANT: Calos, Michele P.
;  APPLICANT:  Sclimenti, Christopher R.
;  TITLE OF INVENTION: ALTERED RECOMBINASES FOR GENOME MODIFICATION
;  FILE REFERENCE: 8400-0011
;  CURRENT APPLICATION NUMBER: US/09/788,297
;  CURRENT FILING DATE:  2001-02-16
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 72
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:T5, oligo 1
US-09-788-297-6

  Query Match             100.0%;  Score 51;  DB 9;  Length 72;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-05;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 52


RESULT 3
US-09-788-297-7/c
; Sequence 7, Application US/09788297
; Patent No. US20020094516A1
; GENERAL INFORMATION:
;  APPLICANT: Calos, Michele P.
;  APPLICANT:  Sclimenti, Christopher R.
;  TITLE OF INVENTION: ALTERED RECOMBINASES FOR GENOME MODIFICATION
;  FILE REFERENCE: 8400-0011
;  CURRENT APPLICATION NUMBER: US/09/788,297
;  CURRENT FILING DATE:  2001-02-16
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 80
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:T5, oligo 2
US-09-788-297-7

  Query Match             100.0%;  Score 51;  DB 9;  Length 80;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-05;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         75 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 25


RESULT 4
US-10-032-393-26
; Sequence 26, Application US/10032393
; Publication No. US20030027286A1
; GENERAL INFORMATION:
;  APPLICANT: Haselbeck, Robert
;  APPLICANT:  Wall, Daniel
;  APPLICANT:  Gross, Molly
;  TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
;  FILE REFERENCE: ELITRA.010A
;  CURRENT APPLICATION NUMBER: US/10/032,393
;  CURRENT FILING DATE:  2001-12-21
;  PRIOR APPLICATION NUMBER: 60/259,434
;  PRIOR FILING DATE: 2000-12-27
;  PRIOR APPLICATION NUMBER: 09/948,993
;  PRIOR FILING DATE: 2001-09-06
;  PRIOR APPLICATION NUMBER: 60/230,335
;  PRIOR FILING DATE: 2000-09-06
;  NUMBER OF SEQ ID NOS: 68
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
;   LENGTH: 80
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Xyl-T5 fusion sequence
US-10-032-393-26

  Query Match             100.0%;  Score 51;  DB 14;  Length 80;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-05;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51


RESULT 5
US-10-032-393-5
; Sequence 5, Application US/10032393
; Publication No. US20030027286A1
; GENERAL INFORMATION:
;  APPLICANT: Haselbeck, Robert
;  APPLICANT:  Wall, Daniel
;  APPLICANT:  Gross, Molly
;  TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
;  FILE REFERENCE: ELITRA.010A
;  CURRENT APPLICATION NUMBER: US/10/032,393
;  CURRENT FILING DATE:  2001-12-21
;  PRIOR APPLICATION NUMBER: 60/259,434
;  PRIOR FILING DATE: 2000-12-27
;  PRIOR APPLICATION NUMBER: 09/948,993
;  PRIOR FILING DATE: 2001-09-06
;  PRIOR APPLICATION NUMBER: 60/230,335
;  PRIOR FILING DATE: 2000-09-06
;  NUMBER OF SEQ ID NOS: 68
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 94
;   TYPE: DNA
;   ORGANISM: Escherichia coli
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide Xyl-T5
US-10-032-393-5

  Query Match             100.0%;  Score 51;  DB 14;  Length 94;
  Best Local Similarity   100.0%;  Pred. No. 2e-05;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 56


RESULT 6
US-10-032-393-6/c
; Sequence 6, Application US/10032393
; Publication No. US20030027286A1
; GENERAL INFORMATION:
;  APPLICANT: Haselbeck, Robert
;  APPLICANT:  Wall, Daniel
;  APPLICANT:  Gross, Molly
;  TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
;  FILE REFERENCE: ELITRA.010A
;  CURRENT APPLICATION NUMBER: US/10/032,393
;  CURRENT FILING DATE:  2001-12-21
;  PRIOR APPLICATION NUMBER: 60/259,434
```

```
;  PRIOR FILING DATE: 2000-12-27
;  PRIOR APPLICATION NUMBER: 09/948,993
;  PRIOR FILING DATE: 2001-09-06
;  PRIOR APPLICATION NUMBER: 60/230,335
;  PRIOR FILING DATE: 2000-09-06
;  NUMBER OF SEQ ID NOS: 68
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 95
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide Xyl-T5 complement
US-10-032-393-6

  Query Match             100.0%;  Score 51;  DB 14;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 2e-05;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 43


RESULT 7
US-10-032-393-1
; Sequence 1, Application US/10032393
; Publication No. US20030027286A1
; GENERAL INFORMATION:
;  APPLICANT: Haselbeck, Robert
;  APPLICANT:  Wall, Daniel
;  APPLICANT:  Gross, Molly
;  TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
;  FILE REFERENCE: ELITRA.010A
;  CURRENT APPLICATION NUMBER: US/10/032,393
;  CURRENT FILING DATE:  2001-12-21
;  PRIOR APPLICATION NUMBER: 60/259,434
;  PRIOR FILING DATE: 2000-12-27
;  PRIOR APPLICATION NUMBER: 09/948,993
;  PRIOR FILING DATE: 2001-09-06
;  PRIOR APPLICATION NUMBER: 60/230,335
;  PRIOR FILING DATE: 2000-09-06
;  NUMBER OF SEQ ID NOS: 68
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 556
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Sequence map showing the Xyl-T5 fusion promoter
;   OTHER INFORMATION: and associated DNA sequences
US-10-032-393-1

  Query Match             100.0%;  Score 51;  DB 14;  Length 556;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-05;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db          6 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 56


RESULT 8
US-10-385-415-2
; Sequence 2, Application US/10385415
; Publication No. US20040014158A1
; GENERAL INFORMATION:
;  APPLICANT: Bacher, Adelbert
;  APPLICANT:  Fischer, Markus
;  TITLE OF INVENTION: PROTEIN CONJUGATES, METHOD, VECTORS, PROTEINS AND DNA FOR
;  TITLE OF INVENTION:  PRODUCING THEM, THEIR USE AND MEDICAMENTS AND VACCINES CONTAININ
;  TITLE OF INVENTION:  A CERTAIN QUANTITIY OF SAID PROTEIN CONJUGATES
;  FILE REFERENCE: 9286.6CT
;  CURRENT APPLICATION NUMBER: US/10/385,415
;  CURRENT FILING DATE:  2003-03-10
;  PRIOR APPLICATION NUMBER: US 09/936,028
;  PRIOR FILING DATE: 2002-01-31
;  PRIOR APPLICATION NUMBER: PCT/EP00/01899
;  PRIOR FILING DATE: 2000-03-03
;  PRIOR APPLICATION NUMBER: DE 19910102.7
;  PRIOR FILING DATE: 1999-03-08
;  NUMBER OF SEQ ID NOS: 154
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 5302
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: p6021-CAT Expression vector
US-10-385-415-2

  Query Match             100.0%;  Score 51;  DB 15;  Length 5302;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-05;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 184


RESULT 9
US-10-385-415-4
; Sequence 4, Application US/10385415
; Publication No. US20040014158A1
; GENERAL INFORMATION:
;  APPLICANT: Bacher, Adelbert
;  APPLICANT:  Fischer, Markus
;  TITLE OF INVENTION: PROTEIN CONJUGATES, METHOD, VECTORS, PROTEINS AND DNA FOR
;  TITLE OF INVENTION:  PRODUCING THEM, THEIR USE AND MEDICAMENTS AND VACCINES CONTAINI
;  TITLE OF INVENTION:  A CERTAIN QUANTITIY OF SAID PROTEIN CONJUGATES
;  FILE REFERENCE: 9286.6CT
;  CURRENT APPLICATION NUMBER: US/10/385,415
;  CURRENT FILING DATE:  2003-03-10
;  PRIOR APPLICATION NUMBER: US 09/936,028
;  PRIOR FILING DATE: 2002-01-31
;  PRIOR APPLICATION NUMBER: PCT/EP00/01899
;  PRIOR FILING DATE: 2000-03-03
;  PRIOR APPLICATION NUMBER: DE 19910102.7
;  PRIOR FILING DATE: 1999-03-08
;  NUMBER OF SEQ ID NOS: 154
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
;   LENGTH: 5767
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: p602-BS-LuSy Expression plasmid
US-10-385-415-4

  Query Match             100.0%;  Score 51;  DB 15;  Length 5767;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-05;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 184


RESULT 10
US-10-032-393-16
; Sequence 16, Application US/10032393
; Publication No. US20030027286A1
; GENERAL INFORMATION:
;  APPLICANT: Haselbeck, Robert
;  APPLICANT:  Wall, Daniel
;  APPLICANT:  Gross, Molly
```

```
;  TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
;  FILE REFERENCE: ELITRA.010A
;  CURRENT APPLICATION NUMBER: US/10/032,393
;  CURRENT FILING DATE:  2001-12-21
;  PRIOR APPLICATION NUMBER: 60/259,434
;  PRIOR FILING DATE: 2000-12-27
;  PRIOR APPLICATION NUMBER: 09/948,993
;  PRIOR FILING DATE: 2001-09-06
;  PRIOR APPLICATION NUMBER: 60/230,335
;  PRIOR FILING DATE: 2000-09-06
;  NUMBER OF SEQ ID NOS: 68
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 6852
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Vector pXyl-T5 p15a
US-10-032-393-16

  Query Match             100.0%;  Score 51;  DB 14;  Length 6852;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-05;
  Matches   51;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1367 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 1417


RESULT 11
US-09-815-242-3094
; Sequence 3094, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
;  APPLICANT: Haselbeck, Robert
;  APPLICANT:  Ohlsen, Kari L.
;  APPLICANT:  Zyskind, Judith W.
;  APPLICANT:  Wall, Daniel
;  APPLICANT:  Trawick, John D.
;  APPLICANT:  Carr, Grant J.
;  APPLICANT:  Yamamoto, Robert T.
;  APPLICANT:  Xu, H. Howard
;  TITLE OF INVENTION: Identification of Essential Genes in
;  TITLE OF INVENTION:  Prokaryotes
;  FILE REFERENCE: ELITRA.011A
;  CURRENT APPLICATION NUMBER: US/09/815,242
;  CURRENT FILING DATE:  2001-03-21
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  NUMBER OF SEQ ID NOS: 14110
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3094
;   LENGTH: 1246
;   TYPE: DNA
;   ORGANISM: Staphylococcus aureus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1246)
;   OTHER INFORMATION: n = A,T,C or G
US-09-815-242-3094

  Query Match             98.0%;  Score 50;  DB 9;  Length 1246;
  Best Local Similarity   98.0%;  Pred. No. 6.3e-05;
  Matches   50;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||||||||| ||||||||||||||||||||||||||
Db         13 TCATAAAAAATTTATTTGCTTTCANGAAAATTTTTCTGTATAATAGATTCA 63


RESULT 12
US-10-032-393-37
; Sequence 37, Application US/10032393
; Publication No. US20030027286A1
; GENERAL INFORMATION:
;  APPLICANT: Haselbeck, Robert
;  APPLICANT:  Wall, Daniel
;  APPLICANT:  Gross, Molly
;  TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
;  FILE REFERENCE: ELITRA.010A
;  CURRENT APPLICATION NUMBER: US/10/032,393
;  CURRENT FILING DATE:  2001-12-21
;  PRIOR APPLICATION NUMBER: 60/259,434
;  PRIOR FILING DATE: 2000-12-27
;  PRIOR APPLICATION NUMBER: 09/948,993
;  PRIOR FILING DATE: 2001-09-06
;  PRIOR APPLICATION NUMBER: 60/230,335
;  PRIOR FILING DATE: 2000-09-06
;  NUMBER OF SEQ ID NOS: 68
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37
;   LENGTH: 51
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Xyl-T5-DD promoter sequence
US-10-032-393-37

  Query Match             84.3%;  Score 43;  DB 14;  Length 51;
  Best Local Similarity   90.2%;  Pred. No. 0.0033;
  Matches   46;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              |||||||||||||||||    |||||||||||||||||||| ||||||||
Db          1 TCATAAAAAATTTATTTTACATCAGGAAAATTTTTCTGTATATTAGATTCA 51


RESULT 13
US-10-032-393-27
; Sequence 27, Application US/10032393
; Publication No. US20030027286A1
; GENERAL INFORMATION:
;  APPLICANT: Haselbeck, Robert
;  APPLICANT:  Wall, Daniel
;  APPLICANT:  Gross, Molly
;  TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
;  FILE REFERENCE: ELITRA.010A
;  CURRENT APPLICATION NUMBER: US/10/032,393
;  CURRENT FILING DATE:  2001-12-21
;  PRIOR APPLICATION NUMBER: 60/259,434
;  PRIOR FILING DATE: 2000-12-27
;  PRIOR APPLICATION NUMBER: 09/948,993
;  PRIOR FILING DATE: 2001-09-06
;  PRIOR APPLICATION NUMBER: 60/230,335
;  PRIOR FILING DATE: 2000-09-06
;  NUMBER OF SEQ ID NOS: 68
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
;   LENGTH: 80
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Xyl-T5-DD fusion sequence
US-10-032-393-27
```

Query Match 84.3%; Score 43; DB 14; Length 80;
Best Local Similarity 90.2%; Pred. No. 0.0036;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              ||||||||||||||||    |||||||||||||||||||| ||||||||
Db          1 TCATAAAAAATTTATTTTACATCAGGAAAATTTTTCTGTATATTAGATTCA 51
```

RESULT 14
US-10-032-393-22
; Sequence 22, Application US/10032393
; Publication No. US20030027286A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Wall, Daniel
; APPLICANT: Gross, Molly
; TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
; FILE REFERENCE: ELITRA.010A
; CURRENT APPLICATION NUMBER: US/10/032,393
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/259,434
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: 09/948,993
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 94
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Xyl-T5-DD
US-10-032-393-22

Query Match 84.3%; Score 43; DB 14; Length 94;
Best Local Similarity 90.2%; Pred. No. 0.0037;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              ||||||||||||||||    |||||||||||||||||||| ||||||||
Db          6 TCATAAAAAATTTATTTTACATCAGGAAAATTTTTCTGTATATTAGATTCA 56
```

RESULT 15
US-10-032-393-23/c
; Sequence 23, Application US/10032393
; Publication No. US20030027286A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Wall, Daniel
; APPLICANT: Gross, Molly
; TITLE OF INVENTION: BACTERIAL PROMOTERS AND METHODS OF USE
; FILE REFERENCE: ELITRA.010A
; CURRENT APPLICATION NUMBER: US/10/032,393
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/259,434
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: 09/948,993
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 95
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Xyl-T5-DD complement

US-10-032-393-23

Query Match 84.3%; Score 43; DB 14; Length 95;
Best Local Similarity 90.2%; Pred. No. 0.0037;
Matches 46; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              ||||||||||||||||    |||||||||||||||||||| ||||||||
Db         93 TCATAAAAAATTTATTTTACATCAGGAAAATTTTTCTGTATATTAGATTCA 43
```

Search completed: April 7, 2004, 05:42:40
Job time : 1006 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: April 7, 2004, 03:21:00 ; Search time 2008 Seconds
(without alignments)
758.452 Million cell updates/sec

Title: US-10-032-393-36
Perfect score: 51
Sequence: 1 tcataaaaaatttatttgct.....ttttctgtataatagattca 51

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	30.2	59.2	318	14	CF350907	CF350907 rl56h06.y
	2	29.4	57.6	358	9	AW049113	AW049113 UI-M-BH1-
c	3	29.4	57.6	534	10	BB365884	BB365884 BB365884
c	4	29.4	57.6	667	10	BB080413	BB080413 BB080413
	5	29.4	57.6	768	13	BQ174160	BQ174160 UI-M-DJ2-
c	6	29.4	57.6	2505	11	AK048039	AK048039 Mus muscu
c	7	29.4	57.6	3403	11	AK034193	AK034193 Mus muscu
	8	29.2	57.3	356	9	AI394884	AI394884 MA001291.
c	9	29.2	57.3	412	9	AA219512	AA219512 zq99g04.r
	10	29	56.9	130	28	BZ128980	BZ128980 CH230-452
	11	29	56.9	595	28	BZ145989	BZ145989 CH230-452
c	12	29	56.9	1048	28	BZ184761	BZ184761 CH230-423
c	13	28.8	56.5	560	28	BZ194126	BZ194126 CH230-465
c	14	28.8	56.5	654	28	BZ216912	BZ216912 CH230-417
c	15	28.8	56.5	773	14	CF406767	CF406767 CH3#044_C
c	16	28.8	56.5	875	28	BZ192372	BZ192372 CH230-465
c	17	28.4	55.7	412	29	AG242333	AG242333 Lotus cor
c	18	28.2	55.3	140	28	AF056259	AF056259 AF056259
c	19	28.2	55.3	611	28	BH741163	BH741163 gt28b09.g
	20	28.2	55.3	733	28	BH957079	BH957079 odj02a12.
	21	28.2	55.3	757	28	BH992006	BH992006 oei11c02.
c	22	28.2	55.3	834	13	BU746323	BU746323 CH3#003_D
c	23	28	54.9	659	14	CB431012	CB431012 606949 MA
	24	28	54.9	729	14	CB430297	CB430297 606181 MA
	25	27.8	54.5	381	10	AW522148	AW522148 UI-R-BO0-
c	26	27.8	54.5	748	28	BH670666	BH670666 BOMBC18TF
	27	27.6	54.1	438	28	AQ782840	AQ782840 HS_5380_B
c	28	27.6	54.1	824	28	BH669814	BH669814 BOMAE23TF
	29	27.4	53.7	571	28	BH506288	BH506288 BOGRV16TF
c	30	27.4	53.7	603	9	AA799484	AA799484 EST188981
	31	27.4	53.7	641	28	BZ082391	BZ082391 lle41b09.
c	32	27.4	53.7	702	29	CE003137	CE003137 tigr-gss-
	33	27.4	53.7	718	28	BH995398	BH995398 oeg92g06.
c	34	27.4	53.7	760	28	BH605836	BH605836 BOGXW23TR
c	35	27.4	53.7	993	28	BH692567	BH692567 BOMJY76TR
	36	27.4	53.7	1340	29	CG751618	CG751618 P046-1-D0
	37	27.2	53.3	101	28	BZ217382	BZ217382 CH230-250
	38	27.2	53.3	292	9	AA365198	AA365198 EST76173
	39	27.2	53.3	357	28	BZ269137	BZ269137 CH230-375
c	40	27.2	53.3	378	28	BZ199225	BZ199225 CH230-495
	41	27.2	53.3	450	29	CE706869	CE706869 tigr-gss-
c	42	27.2	53.3	544	28	BZ217207	BZ217207 CH230-372
	43	27.2	53.3	546	28	BZ177519	BZ177519 CH230-493
	44	27.2	53.3	560	28	BZ214923	BZ214923 CH230-466
c	45	27.2	53.3	631	28	BZ219091	BZ219091 CH230-259

ALIGNMENTS

RESULT 1
CF350907
LOCUS CF350907 318 bp mRNA linear EST 20-AUG-2003
DEFINITION rl56h06.y1 Meloidogyne javanica J2 SMART pGEM Meloidogyne javanica cDNA 5', mRNA sequence.
ACCESSION CF350907
VERSION CF350907.1 GI:33953420
KEYWORDS EST.
SOURCE Meloidogyne javanica (root-knot nematode)
ORGANISM Meloidogyne javanica
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.
REFERENCE 1 (bases 1 to 318)
AUTHORS McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
TITLE The Washington Univ. Nematode EST Project, 1999
JOURNAL Unpublished (1999)
COMMENT Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800

Fax: 314 286 1810
Email: est@watson.wustl.edu
Cloned unidirectionally. Poly(A)+ RNA was concentrated and purified using Dynabeads (Dynal) and mRNA eluted for first strand synthesis. First strand cDNA was created using MMLV RT (Powerscript, Clontech) and primed with oligo(dT) with XhoI site and 5'SMART 'anchor' added using chimeric DNA-RNA oligo. 12 PCR cycles were done using first strand and primers specific to SMART oligo and 3' end. Double stranded cDNA was digested using XhoI/NotI, fractioned on Chroma-spin 400 columns (Clontech) and ligated to digested pGEM-11zf(+) plasmid. Chemically competent DH10B cells were used as host cells. Library materials provided by Dr. David Bird of North Carolina State University. Library construction by Jeff Rousch. See www.nematode.net for additional project information.
Putative full length read
The vector to vector length is 319
Seq primer: Sp6.

```
FEATURES             Location/Qualifiers
     source          1. .318
                     /organism="Meloidogyne javanica"
                     /mol_type="mRNA"
                     /db_xref="taxon:6303"
                     /tissue_type="whole organism"
                     /dev_stage="J2"
                     /lab_host="DH10B"
                     /clone_lib="Meloidogyne javanica J2 SMART pGEM"
                     /note="Vector: plasmid (ampicillin resistant); Site_1:
                     XhoI; Site_2: NotI; Cloned unidirectionally. Poly(A)+ RNA
                     was concentrated and purified using Dynabeads (Dynal) and
                     mRNA eluted for first strand synthesis. First strand cDNA
                     was created using MMLV RT (Powerscript, Clontech) and
                     primed with oligo(dT) with XhoI site and 5'SMART 'anchor'
                     added using chimeric DNA-RNA oligo. 12 PCR cycles were
                     done using first strand and primers specific to SMART
                     oligo and 3' end. Double stranded cDNA was digested using
                     XhoI/NotI, fractioned on Chroma-spin 400 columns
                     (Clontech) and ligated to digested pGEM-11zf(+) plasmid.
                     Chemically competent DH10B cells were used as host cells.
                     Library materials provided by Dr. David Bird of North
                     Carolina State University. Library construction by Jeff
                     Rousch. See www.nematode.net for additional project
                     information."
ORIGIN
```

```
  Query Match             59.2%;  Score 30.2;  DB 14;  Length 318;
  Best Local Similarity   81.4%;  Pred. No. 2.9e+02;
  Matches   35;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          2 CATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAAT 44
              || ||| |||||||||  | ||||| || |||||||||| ||||
Db         80 CAAAAAGAATTTATTTTATATCAGGGAATTTTTTCTGTTTAAT 122
```

```
RESULT 2
AW049113
LOCUS       AW049113                358 bp    mRNA    linear   EST 18-SEP-1999
DEFINITION  UI-M-BH1-amt-g-11-0-UI.s1 NIH_BMAP_M_S2 Mus musculus cDNA clone
            UI-M-BH1-amt-g-11-0-UI 3', mRNA sequence.
ACCESSION   AW049113
VERSION     AW049113.1  GI:5909642
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 358)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: Chin, H
            National Institute of Mental Health
            6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
            20892-9643, USA
            Tel: 301 443 1706
            Fax: 301 443 9890
            Email: mEST@mail.nih.gov
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. The sequence tag present in the cDNA between the NotI site
            and the oligo-dT track served to identify it as a clone from the
            normalized basal ganglia library cDNA Library Preparation: M.B.
            Soares Lab Clone distribution: NIH BMAP cDNA clones will be made
            available by the means that is soon to be determined. When NIH
            determines the means for distribution of the BMAP cDNA clones, this
            record will be updated accordingly when that means is determined.
            The following repetitive elements were found in this cDNA sequence:
            15-92, >(TA)n#Simple_repeat
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .358
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UI-M-BH1-amt-g-11-0-UI"
                     /dev_stage="27-32 days"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NIH_BMAP_M_S2"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The
                     NIH_BMAP_M_S2 library is a subtracted library derived from
                     NIH_BMAP_M_S1, which in turn is a subtracted library
                     derived from a mixture of normalized libraries from ten
                     regions of the mouse brain (cerebellum, brain stems,
                     olfactory bulbs, hypothalamus, cortex, amygdala, basal
                     ganglia, pineal gland, striatum, hipoccampus). The driver
                     used for subtraction consisted of a pool of 5,000 clones
                     from the NIH_BMAP_M_S1 library and a pool of 2,000 clones
                     obtained from non-normalized and normalized mouse brain
                     spinal cord libraries.
                     TAG_TISSUE=basal-ganglia
                     TAG_LIB=NIH_BMAP_M_S2
                     TAG_SEQ=TGTAC"
ORIGIN
```

```
  Query Match             57.6%;  Score 29.4;  DB 9;  Length 358;
  Best Local Similarity   76.6%;  Pred. No. 4.5e+02;
  Matches   36;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          3 ATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATT 49
              |||| | |||||||||| | ||| || |||| | | ||| ||| |||
Db         20 ATAATATATTTATTTGCATACAGAAATATTTATTTCTATTATACATT 66
```

```
RESULT 3
BB365884/c
LOCUS       BB365884                534 bp    mRNA    linear   EST 24-OCT-2001
DEFINITION  BB365884 RIKEN full-length enriched, 16 days embryo head Mus
            musculus cDNA clone C130031F03 3', mRNA sequence.
ACCESSION   BB365884
VERSION     BB365884.2  GI:16406384
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 534)
  AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
            Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
            Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
            Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
```

Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
JOURNAL Unpublished (2001)
COMMENT On Jul 12, 2000 this sequence version replaced gi:9077712.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
FEATURES Location/Qualifiers
source 1. .534
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="C130031F03"
/sex="mixed"
/tissue_type="head"
/dev_stage="16 days embryo"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 16 days embryo head"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I"

ORIGIN

Query Match 57.6%; Score 29.4; DB 10; Length 534;
Best Local Similarity 76.6%; Pred. No. 3.9e+02;
Matches 36; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 3 ATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATT 49
Db 305 ATAATATATTTATTTGCATACAGAAATATTTATTTCTATTATACATT 259

RESULT 4
BB080413/c
LOCUS BB080413 667 bp mRNA linear EST 18-OCT-2001
DEFINITION BB080413 RIKEN full-length enriched, adult male diencephalon Mus musculus cDNA clone 9330162L04 3', mRNA sequence.
ACCESSION BB080413
VERSION BB080413.2 GI:16260594
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 667)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
JOURNAL Unpublished (2001)
COMMENT On Jun 21, 2000 this sequence version replaced gi:8645473.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
FEATURES Location/Qualifiers

```
     source          1. .667
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="9330162L04"
                     /sex="male"
                     /tissue_type="diencephalon"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="RIKEN full-length enriched, adult male
                     diencephalon"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. cDNA went through one round of normalization
                     to Rot = 10.0 and subtraction to Rot = 185.0. Second
                     strand cDNA was prepared with the primer adapter of
                     sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC
                     3']. cDNA was cloned into the XhoI and BamHI sites.
                     Vector: a modified pBluescript KS(+) after bulk excision
                     from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
                     BamHI"
ORIGIN

  Query Match             57.6%;  Score 29.4;  DB 10;  Length 667;
  Best Local Similarity   76.6%;  Pred. No. 3.7e+02;
  Matches   36;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          3 ATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATT 49
              |||| | |||||||||| | ||| || |||| | | ||| ||| |||
Db        662 ATAATATATTTATTTGCATACAGAAATATTTATTTCTATTATACATT 616


RESULT 5
BQ174160
LOCUS       BQ174160                768 bp    mRNA    linear   EST 30-APR-2002
DEFINITION  UI-M-DJ2-bvw-c-09-0-UI.s1 NIH_BMAP_DJ2 Mus musculus cDNA clone
            UI-M-DJ2-bvw-c-09-0-UI 3', mRNA sequence.
ACCESSION   BQ174160
VERSION     BQ174160.1  GI:20349651
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 768)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: Chin, H
            National Institute of Mental Health
            6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
            20892-9643, USA
            Tel: 301 443 1706
            Fax: 301 443 9890
            Email: mEST@mail.nih.gov
            Tissue Procurement: Dr. Robin Davisson
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
             The following repetitive elements were found in this cDNA
            sequence: 16-93, >(TA)n#Simple_repeat
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .768
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="UI-M-DJ2-bvw-c-09-0-UI"
                     /tissue_type="subfornical organ and postrema"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="NIH_BMAP_DJ2"
                     /note="Organ: brain; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-M-DJ2 is a subtracted cDNA library constructed
                     according to Bonaldo, Lennon and Soares, Genome Research,
                     6:791-806, 1996. First strand cDNA synthesis was primed
                     with an oligo-dT primer containing a Not I site. Double
                     stranded cDNA was ligated to an EcoR I adaptor, digested
                     with Not I, and cloned directionally into pT7T3-Pac
                     vector. The oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tag for this library is: GCTACATGAT, subfornical
                     organ and area postrema.
                     TAG_TISSUE=subfornical organ and postrema
                     TAG_LIB=UI-M-DJ2
                     TAG_SEQ=GCTACATGAT"
ORIGIN

  Query Match             57.6%;  Score 29.4;  DB 13;  Length 768;
  Best Local Similarity   76.6%;  Pred. No. 3.5e+02;
  Matches   36;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          3 ATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATT 49
              |||| | |||||||||| | ||| || |||| | | ||| ||| |||
Db         21 ATAATATATTTATTTGCATACAGAAATATTTATTTCTATTATACATT 67


RESULT 6
AK048039/c
LOCUS       AK048039                2505 bp    mRNA    linear   HTC 20-SEP-2003
DEFINITION  Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched
            library, clone:C130031F03 product:unknown EST, full insert
            sequence.
ACCESSION   AK048039
VERSION     AK048039.1  GI:26092610
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
```

```
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 2505)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.go.jp/
            URL:http://fantom.gsc.riken.go.jp/.
FEATURES             Location/Qualifiers
     source          1. .2505
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="FANTOM_DB:C130031F03"
                     /db_xref="MGI:2414069"
                     /db_xref="taxon:10090"
                     /clone="C130031F03"
                     /tissue_type="head"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="16 days embryo"
     misc_feature    1. .2505
                     /note="unknown EST (GB|BI735511, evidence: BLASTN, 99%,
                     match=817)"
ORIGIN

  Query Match           57.6%;  Score 29.4;  DB 11;  Length 2505;
  Best Local Similarity   76.6%;  Pred. No. 2.3e+02;
  Matches   36;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          3 ATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATT 49
              |||| | |||||||||| | ||| || |||| | | ||| ||| |||
Db       2274 ATAATATATTTATTTGCATACAGAAATATTTATTTCTATTATACATT 2228
```

```
RESULT 7
AK034193/c
LOCUS       AK034193                3403 bp    mRNA    linear   HTC 18-SEP-2003
DEFINITION  Mus musculus adult male diencephalon cDNA, RIKEN full-length
            enriched library, clone:9330162L04 product:unknown EST, full insert
            sequence.
ACCESSION   AK034193
VERSION     AK034193.1  GI:26083816
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 3403)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
```

```
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.go.jp/
            URL:http://fantom.gsc.riken.go.jp/.
FEATURES              Location/Qualifiers
     source           1. .3403
                      /organism="Mus musculus"
                      /mol_type="mRNA"
                      /strain="C57BL/6J"
                      /db_xref="FANTOM_DB:9330162L04"
                      /db_xref="MGI:2398388"
                      /db_xref="taxon:10090"
                      /clone="9330162L04"
                      /sex="male"
                      /tissue_type="diencephalon"
                      /clone_lib="RIKEN full-length enriched mouse cDNA library"
                      /dev_stage="adult"
     misc_feature     1. .3403
                      /note="unknown EST (GB|BI735511, evidence: BLASTN, 99%,
                      match=817)"
ORIGIN

  Query Match             57.6%;  Score 29.4;  DB 11;  Length 3403;
  Best Local Similarity   76.6%;  Pred. No. 2.1e+02;
  Matches   36;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          3 ATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATT 49
              |||| | |||||||||| | ||| || |||| | | ||| ||| |||
Db       3391 ATAATATATTTATTTGCATACAGAAATATTTATTTCTATTATACATT 3345


RESULT 8
AI394884
LOCUS       AI394884                356 bp    mRNA    linear   EST 04-FEB-1999
DEFINITION  MA001291.C8F Soares normalized S8W Schistosoma mansoni cDNA 3',
            mRNA sequence.
ACCESSION   AI394884
VERSION     AI394884.1  GI:4224431
KEYWORDS    EST.
SOURCE      Schistosoma mansoni
  ORGANISM  Schistosoma mansoni
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
REFERENCE   1  (bases 1 to 356)
  AUTHORS   Bailey,J.A., Bentley,K., Blanton,R.E., Soares,M.B. and
            Chakravarti,A.
  TITLE     Expressed sequence tags from a normalized adult Schistosoma mansoni
            library
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Chakravarti A
            Department of Genetics
            Case Western Reserve University
            2109 Adelbert Rd, Cleveland, OH 44106, USA
            Tel: 216-368-5847
            Fax: 216-368-5857
            Email: axc39@po.cwru.edu
            Additional data regarding this EST may be found at
            http://genome.cwru.edu/schistosoma/est/S8West.html
            Seq primer: M13 Forward.
FEATURES              Location/Qualifiers
     source           1. .356
                      /organism="Schistosoma mansoni"
                      /mol_type="mRNA"
                      /strain="Puerto Rican"
                      /db_xref="taxon:6183"
                      /sex="mixed"
                      /dev_stage="8 week old adult worms"
                      /lab_host="Mus musculus"
                      /clone_lib="Soares normalized S8W"
                      /note="Vector: pT7T3-pac; Site_1: NotI; Site_2: EcoRI;
                      Note: normalization has resulted in an increased frequency
                      of the rare contaminating mouse (host) sequences (~10%).
                      For details of library construction see:  Bonaldo MF,
                      Lennon G, Soares MB. Normalization and Subtraction: Two
                      Approaches to Facilitate Gene Discovery. 1996. Genome
                      Research 6:791-806"
ORIGIN

  Query Match             57.3%;  Score 29.2;  DB 9;  Length 356;
  Best Local Similarity   74.0%;  Pred. No. 5.1e+02;
  Matches   37;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          2 CATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              ||| |||||| || ||  | | |  |||||| ||||||  ||||||||
Db        140 CATTAAAAATCTAATTCTTCTAAACAAAATTCTTCTGTGAAATAGATTAA 189


RESULT 9
AA219512/c
LOCUS       AA219512                412 bp    mRNA    linear   EST 07-FEB-1997
DEFINITION  zq99g04.r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens
            cDNA clone IMAGE:650166 5', mRNA sequence.
ACCESSION   AA219512
VERSION     AA219512.1  GI:1833571
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 412)
  AUTHORS   Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
            Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
            Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
            Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
            Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,
            Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
            and Marra,M.
  TITLE     Generation and analysis of 280,000 human expressed sequence tags
  JOURNAL   Genome Res. 6 (9), 807-828 (1996)
  MEDLINE   97044478
   PUBMED   8889549
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -28m13 rev1 ET from Amersham
            High quality sequence stop: 262.
FEATURES              Location/Qualifiers
     source           1. .412
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="GDB:5276755"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:650166"
                      /tissue_type="neuroepithelial cells"
                      /dev_stage="Ntera-2 neuroepithelial cells"
                      /lab_host="SOLR (kanamycin resistant)"
                      /clone_lib="Stratagene NT2 neuronal precursor 937230"
                      /note="Organ: brain; Vector: pBluescript SK-; Site_1:
                      EcoRI; Site_2: XhoI; Cloned unidirectionally.  Primer:
                      Oligo dT. Uninduced, exponentially growing neuroepithelial
                      cells (Ntera-2/c1.D1). Average insert size: 1.0 kb;
                      Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGCACGAG
                      3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTT 3'"
ORIGIN

  Query Match             57.3%;  Score 29.2;  DB 9;  Length 412;
```

```
  Best Local Similarity   72.5%;  Pred. No. 4.8e+02;
  Matches   37;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 TCATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATTCA 51
              || ||||||  | |||| |||||   ||||||| | |||||  || ||| |
Db        122 TCNTAAAAAGATGATTTTCTTTCTTAAAAATTTCTGTGTATTCTAAATTTA 72


RESULT 10
BZ128980
LOCUS       BZ128980                130 bp    DNA     linear   GSS 11-OCT-2002
DEFINITION  CH230-452M22.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone
            CH230-452M22, genomic survey sequence.
ACCESSION   BZ128980
VERSION     BZ128980.1  GI:23769927
KEYWORDS    GSS.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 130)
  AUTHORS   Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,
            Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D.,
            Riggs,F., de Jong,P. and Fraser,C.M.
  TITLE     Rat BAC End Sequences from Library CHORI-230 MboI segment
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the rat BAC library CHORI-230
            (http://www.chori.org/bacpac/rat230.htm). For BAC library
            availability, please contact Pieter de Jong (pdejong@mail.cho.org).
            Clones may be purchased from BACPAC Resources
            (http://www.chori.org/bacpac/or ering_information.htm). BAC end
            page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
            Plate: 452  row: M  column: 22
            Seq primer: SP6
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .130
                     /organism="Rattus norvegicus"
                     /mol_type="genomic DNA"
                     /strain="BN/SsNHsd/MCW"
                     /db_xref="taxon:10116"
                     /clone="CH230-452M22"
                     /sex="Female"
                     /cell_type="Brain"
                     /clone_lib="CHORI-230 Segment 2"
                     /note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
                     CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
                     Pieter de Jong"
ORIGIN

  Query Match            56.9%;  Score 29;  DB 28;  Length 130;
  Best Local Similarity  86.5%;  Pred. No. 8e+02;
  Matches   32;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          5 AAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTAT 41
              ||||| |||  |||| |||| ||||||||||||||||
Db         10 AAAAATTTTGATTGCATTCATGAAAATTTTTCTGTAT 46


RESULT 11
BZ145989
LOCUS       BZ145989                595 bp    DNA     linear   GSS 11-OCT-2002
DEFINITION  CH230-452N22.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone
            CH230-452N22, genomic survey sequence.
ACCESSION   BZ145989
VERSION     BZ145989.1  GI:23786936
KEYWORDS    GSS.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 595)
  AUTHORS   Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,
            Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D.,
            Riggs,F., de Jong,P. and Fraser,C.M.
  TITLE     Rat BAC End Sequences from Library CHORI-230 MboI segment
  JOURNAL   Unpublished (1999)
COMMENT     Other_GSSs: CH230-452N22.TV
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the rat BAC library CHORI-230
            (http://www.chori.org/bacpac/rat230.htm). For BAC library
            availability, please contact Pieter de Jong (pdejong@mail.cho.org).
            Clones may be purchased from BACPAC Resources
            (http://www.chori.org/bacpac/or ering_information.htm). BAC end
            page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
            Plate: 452  row: N  column: 22
            Seq primer: SP6
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .595
                     /organism="Rattus norvegicus"
                     /mol_type="genomic DNA"
                     /strain="BN/SsNHsd/MCW"
                     /db_xref="taxon:10116"
                     /clone="CH230-452N22"
                     /sex="Female"
                     /cell_type="Brain"
                     /clone_lib="CHORI-230 Segment 2"
                     /note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
                     CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
                     Pieter de Jong"
ORIGIN

  Query Match            56.9%;  Score 29;  DB 28;  Length 595;
  Best Local Similarity  86.5%;  Pred. No. 4.8e+02;
  Matches   32;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          5 AAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTAT 41
              ||||| |||  |||| |||| ||||||||||||||||
Db        485 AAAAATTTTGATTGCATTCATGAAAATTTTTCTGTAT 521


RESULT 12
BZ184761/c
LOCUS       BZ184761               1048 bp    DNA     linear   GSS 11-OCT-2002
DEFINITION  CH230-423F16.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone
            CH230-423F16, genomic survey sequence.
ACCESSION   BZ184761
VERSION     BZ184761.1  GI:23834700
KEYWORDS    GSS.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 1048)
  AUTHORS   Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,
            Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D.,
            Riggs,F., de Jong,P. and Fraser,C.M.
  TITLE     Rat BAC End Sequences from Library CHORI-230 MboI segment
  JOURNAL   Unpublished (1999)
```

```
COMMENT     Other_GSSs: CH230-423F16.TV
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the rat BAC library CHORI-230
            (http://www.chori.org/bacpac/rat230.htm). For BAC library
            availability, please contact Pieter de Jong (pdejong@mail.cho.org).
            Clones may be purchased from BACPAC Resources
            (http://www.chori.org/bacpac/or ering_information.htm). BAC end
            page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
            Plate: 423  row: F  column: 16
            Seq primer: SP6
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .1048
                     /organism="Rattus norvegicus"
                     /mol_type="genomic DNA"
                     /strain="BN/SsNHsd/MCW"
                     /db_xref="taxon:10116"
                     /clone="CH230-423F16"
                     /sex="Female"
                     /cell_type="Brain"
                     /clone_lib="CHORI-230 Segment 2"
                     /note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
                     CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
                     Pieter de Jong"
ORIGIN

  Query Match             56.9%;  Score 29;  DB 28;  Length 1048;
  Best Local Similarity   86.5%;  Pred. No. 4e+02;
  Matches   32;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          5 AAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTAT 41
              ||||| |||  |||| |||| ||||||||||||||||
Db        108 AAAAATTTTGATTGCATTCATGAAAATTTTTCTGTAT 72


RESULT 13
BZ194126/c
LOCUS       BZ194126                560 bp    DNA     linear   GSS 11-OCT-2002
DEFINITION  CH230-465D15.TJB CHORI-230 Segment 2 Rattus norvegicus genomic
            clone CH230-465D15, genomic survey sequence.
ACCESSION   BZ194126
VERSION     BZ194126.1  GI:23852178
KEYWORDS    GSS.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 560)
  AUTHORS   Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,
            Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D.,
            Riggs,F., de Jong,P. and Fraser,C.M.
  TITLE     Rat BAC End Sequences from Library CHORI-230 MboI segment
  JOURNAL   Unpublished (1999)
COMMENT     Other_GSSs: CH230-465D15.TVB
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the rat BAC library CHORI-230
            (http://www.chori.org/bacpac/rat230.htm). For BAC library
            availability, please contact Pieter de Jong (pdejong@mail.cho.org).
            Clones may be purchased from BACPAC Resources
            (http://www.chori.org/bacpac/or ering_information.htm). BAC end
            page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
            Plate: 465  row: D  column: 15
            Seq primer: SP6
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .560
                     /organism="Rattus norvegicus"
                     /mol_type="genomic DNA"
                     /strain="BN/SsNHsd/MCW"
                     /db_xref="taxon:10116"
                     /clone="CH230-465D15"
                     /sex="Female"
                     /cell_type="Brain"
                     /clone_lib="CHORI-230 Segment 2"
                     /note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
                     CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
                     Pieter de Jong"
ORIGIN

  Query Match             56.5%;  Score 28.8;  DB 28;  Length 560;
  Best Local Similarity   82.5%;  Pred. No. 5.5e+02;
  Matches   33;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          2 CATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTAT 41
              | || ||| |||| || | |||| ||||||||||||||||
Db        526 CCTAGAAATTTTAATTCCATTCATGAAAATTTTTCTGTAT 487


RESULT 14
BZ216912/c
LOCUS       BZ216912                654 bp    DNA     linear   GSS 11-OCT-2002
DEFINITION  CH230-417O3.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone
            CH230-417O3, genomic survey sequence.
ACCESSION   BZ216912
VERSION     BZ216912.1  GI:23875270
KEYWORDS    GSS.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 654)
  AUTHORS   Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K.,
            Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D.,
            Riggs,F., de Jong,P. and Fraser,C.M.
  TITLE     Rat BAC End Sequences from Library CHORI-230 MboI segment
  JOURNAL   Unpublished (1999)
COMMENT     Other_GSSs: CH230-417O3.TV
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the rat BAC library CHORI-230
            (http://www.chori.org/bacpac/rat230.htm). For BAC library
            availability, please contact Pieter de Jong (pdejong@mail.cho.org).
            Clones may be purchased from BACPAC Resources
            (http://www.chori.org/bacpac/or ering_information.htm). BAC end
            page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
            Plate: 417  row: O  column: 3
            Seq primer: SP6
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .654
                     /organism="Rattus norvegicus"
                     /mol_type="genomic DNA"
                     /strain="BN/SsNHsd/MCW"
                     /db_xref="taxon:10116"
                     /clone="CH230-417O3"
                     /sex="Female"
                     /cell_type="Brain"
```

/clone_lib="CHORI-230 Segment 2"
/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
Pieter de Jong"
ORIGIN

Query Match 56.5%; Score 28.8; DB 28; Length 654;
Best Local Similarity 82.5%; Pred. No. 5.2e+02;
Matches 33; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 CATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTAT 41
Db 513 CTTAGAAATTTTAATTCCATTCATGAAAATTTTTCTGTAT 474

RESULT 15
CF406767/c
LOCUS CF406767 773 bp mRNA linear EST 02-SEP-2003
DEFINITION CH3#044_C08T3 Canine heart normalized cDNA Library in pBluescript
Canis familiaris cDNA clone CH3#044_C08 3', mRNA sequence.
ACCESSION CF406767
VERSION CF406767.1 GI:34407011
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 773)
AUTHORS Yi,Y., Desai,R., Olarte,M., Henthorn,P. and George A.L.
TITLE Expressed sequence tags from Canine heart
JOURNAL Unpublished (2003)
COMMENT Other_ESTs: CH3#044_C08T7
Contact: George AL
Division of Genetic Medicine
Vanderbilt University
529 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA
Tel: 615 936 2660
Fax: 615 936 2661
Email: al.george@vanderbilt.edu
Insert Length: 1448 Std Error: 0.00
Seq primer: T3: ATTAACCCTCACTAAAGGGA
High quality sequence start: 64
High quality sequence stop: 733.
FEATURES Location/Qualifiers
source 1. .773
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/clone="CH3#044_C08"
/tissue_type="heart"
/cell_type="heart"
/dev_stage="mixed developmental stages (adult, 30 day - 40
day fetal)"
/clone_lib="Canine heart normalized cDNA Library in
pBluescript"
/note="Organ: heart; Vector: pBluescript; Site_1: 5' of
vector NotI; Site_2: 3' of vector EcoRI; Tissue source:
dog heart (adult, 30 day - 40 day fetal), right and left
atria and ventricle. Dog breed - mixed (beagle, German
shepherd, pointer, Irish setter). Library construction:
oligo-dT primed"
ORIGIN

Query Match 56.5%; Score 28.8; DB 14; Length 773;
Best Local Similarity 75.0%; Pred. No. 4.9e+02;
Matches 36; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 2 CATAAAAAATTTATTTGCTTTCAGGAAAATTTTTCTGTATAATAGATT 49
Db 238 CTTAAAAAATTTTTTAGTGTATAGAATAATTTTTCTATATGATAGACT 191

Search completed: April 7, 2004, 05:25:48

Job time : 2013 secs